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OM protein - protein search, using sw model

Run on: October 18, 2002, 10:33:53 ; Search time 13 Seconds
(without alignments)
319.412 Million cell updates/sec

Title: US-09-218-913D-52

Perfect score: 948

Sequence: 1 ADPRSHDFCLVSKVWGRC.....ACMLRCFRQENPPLGLGSK 170

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 231628 seqs, 24425594 residues

Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued_Patents_AA.*

- 1: /cgn2_6/ptodata/1/1aa/5A_COMB.pep.*
- 2: /cgn2_6/ptodata/1/1aa/5B_COMB.pep.*
- 3: /cgn2_6/ptodata/1/1aa/6A_COMB.pep.*
- 4: /cgn2_6/ptodata/1/1aa/6B_COMB.pep.*
- 5: /cgn2_6/ptodata/1/1aa/PCTUS_COMB.pep.*
- 6: /cgn2_6/ptodata/1/1aa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	948	100.0	252	1	US-08-685-660A-7
2	948	100.0	252	2	US-08-974-196-7
3	948	100.0	252	4	US-09-071-709-10
4	948	100.0	252	4	US-09-013-896A-2
5	312	32.9	513	4	US-08-685-558A-18
6	299.5	31.6	348	4	US-09-071-709-2
7	297	31.3	51	4	US-09-013-896A-10
8	297	31.3	51	4	US-09-013-896A-11
9	247.5	26.1	122	2	US-08-422-333-12
10	247.5	26.1	122	6	5187153-20
11	247.5	26.1	122	6	5220013-23
12	244.5	25.8	143	2	US-08-422-333-10
13	244.5	25.8	143	6	5223482-20
14	244.5	25.8	144	6	5187153-18
15	244.5	25.8	147	1	US-08-358-160-72
16	243.5	25.7	127	6	5466783-24
17	241.5	25.5	123	6	5466783-21
18	233.5	24.6	122	6	5223482-22
19	233.5	24.6	276	1	US-07-828-920A-1
20	233.5	24.6	276	1	US-08-437-841-9
21	233.5	24.6	276	1	US-08-286-521-9
22	233.5	24.6	276	1	US-08-436-175-9
23	233.5	24.6	276	2	US-08-796-850-1
24	233.5	24.6	276	3	US-08-854-764-3
25	233.5	24.6	276	4	US-08-943-682-9
26	233.5	24.6	276	5	PCT-US95-09377-3
27	233.5	24.6	276	5	PCT-US95-09464-9

ALIGNMENTS

RESULT 1

US-08-685-660A-7

; Sequence 7, Application US/08685660A

; Patent No. 5731412

; GENERAL INFORMATION:

; APPLICANT: SHIMOMURA, Takeshi

; APPLICANT: KAWAGUCHI, Toshiya

; APPLICANT: KITAMURA, Naomi

; TITLE OF INVENTION: NOVEL PROTEIN, DNA CODING FOR SAME

; TITLE OF INVENTION: AND METHOD OF PRODUCING THE PROTEIN

; NUMBER OF SEQUENCES: 7

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: SUGHRUE, MION, ZINN, MACPEAK & SEAS

; STREET: 2100 Pennsylvania Avenue, N.W.

; CITY: Washington

; STATE: DC

; COUNTRY: USA

; ZIP: 20037

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/685,660A

; FILING DATE: 24-JUL-1996

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: JPA Hei 7-187134

; FILING DATE: 24-JUL-1995

; ATTORNEY/AGENT INFORMATION:

; NAME: KIT, Gordon

; REGISTRATION NUMBER: 30,764

; REFERENCE/DOCKET NUMBER: Q-42295

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (202) 293-7060

; TELEFAX: (202) 293-7860

; INFORMATION FOR SEQ ID NO: 7:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 252 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

; US-08-685-660A-7

Query Match 100.0%; Score 948; DB 1; Length 252;

Best Local Similarity 100.0%; Pred. No. 3.1e-92;

Matches 170; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADPRSHDFCLVSKVWGRCASMPRWNYVTGSCQLFVYGGCDGNSNNYTKKECLKK 60

|||||

Sequence 1, Appli
Sequence 2, Appli
Sequence 9, Appli
Sequence 18, Appli
Sequence 18, Appli
Sequence 1, Appli
Sequence 25, Appli
Sequence 1, Appli
Sequence 1, Appli
Sequence 2, Appli
Sequence 25, Appli
Patent No. 5466783
Sequence 2, Appli
Sequence 2, Appli
Patent No. 5466783
Sequence 19, Appli
Sequence 19, Appli
Sequence 19, Appli

277 1 US-07-844-297-1
304 1 US-08-026-145-2
304 1 US-08-446-646-9
304 1 US-08-676-125A-18
304 2 US-09-136-012A-18
304 3 US-08-676-124-1
304 3 US-08-208-264A-25
304 3 US-09-414-878-1
304 3 US-09-240-136-1
304 4 US-09-054-782-2
304 4 US-09-421-097-25
304 6 5466783-2
352 3 US-08-854-764-2
352 5 PCT-US95-09377-2
123 6 5466783-22
161 1 US-08-437-841-19
161 1 US-08-286-521-19
161 1 US-08-436-175-19

28 233.5 24.6
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33 233.5 24.6
34 233.5 24.6
35 233.5 24.6
36 233.5 24.6
37 233.5 24.6
38 233.5 24.6
39 233.5 24.6
40 233.5 24.6
41 233.5 24.6
42 233.5 24.5
43 232 24.5
44 232 24.5
45 232 24.5

Db 28 ADERSIHDFCLVSKVGRASMPRWYNTDGSQCLFVYGGDGNNSNYLTKEECLKK 87
Qy 61 CATVTENATGDLATSRNAADSSVPSAPRRQDSEHSDMFNVEEYCTANAVTGPCRASFP 120
Db 88 CATVTENATGDLATSRNAADSSVPSAPRRQDSEHSDMFNVEEYCTANAVTGPCRASFP 147
Qy 121 RWFYDVERNSCNFIYGGCRGNKNSYRSEAEACMLRCFRQENPPLPLGSK 170
Db 148 RWFYDVERNSCNFIYGGCRGNKNSYRSEAEACMLRCFRQENPPLPLGSK 197

RESULT 2
US-08-974-196-7
; Sequence 7, Application US/08974196
; Patent No. 5854396
; GENERAL INFORMATION:
; APPLICANT: SHIMOMURA, Takeshi
; APPLICANT: KAWAGUCHI, Toshiya
; APPLICANT: KITAMURA, Naomi
; TITLE OF INVENTION: NOVEL PROTEIN, DNA CODING FOR SAME
; TITLE OF INVENTION: AND METHOD OF PRODUCING THE PROTEIN
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SUGHRUE, MION, ZINN, MACPEAK & SEAS
; STREET: 2100 Pennsylvania Avenue, N.W.
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/974.196
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/685.660
; FILING DATE: 24-JUL-1996
; APPLICATION NUMBER: JPA Hei 7-187134
; FILING DATE: 24-JUL-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: KIT, Gordon
; REGISTRATION NUMBER: 30,764
; REFERENCE/DOCKET NUMBER: Q-42295
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 293-7060
; TELEFAX: (202) 293-7860
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 252 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-974-196-7

Query Match 100.0%; Score 948; DB 2; Length 252;
Best Local Similarity 100.0%; Pred. No. 3.1e-92;
Matches 170; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ADERSIHDFCLVSKVGRASMPRWYNTDGSQCLFVYGGDGNNSNYLTKEECLKK 60
Db 28 ADERSIHDFCLVSKVGRASMPRWYNTDGSQCLFVYGGDGNNSNYLTKEECLKK 87
Qy 61 CATVTENATGDLATSRNAADSSVPSAPRRQDSEHSDMFNVEEYCTANAVTGPCRASFP 120
Db 88 CATVTENATGDLATSRNAADSSVPSAPRRQDSEHSDMFNVEEYCTANAVTGPCRASFP 147
Qy 121 RWFYDVERNSCNFIYGGCRGNKNSYRSEAEACMLRCFRQENPPLPLGSK 170
Db 148 RWFYDVERNSCNFIYGGCRGNKNSYRSEAEACMLRCFRQENPPLPLGSK 197

RESULT 3
US-09-071-709-10
; Sequence 10, Application US/09071709
; Patent No. 6171790
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Tang, Y. Tom
; APPLICANT: Lal, Preeti
; APPLICANT: Corley, Neil C.
; APPLICANT: Guegler, Karl J.
; APPLICANT: Patterson, Chandra
; TITLE OF INVENTION: HUMAN PROTEASE ASSOCIATED PROTEINS
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
; STREET: 3174 PORTER DRIVE
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/071.709
; FILING DATE: Filed Herewith
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: CERRONE, MICHAEL C.
; REGISTRATION NUMBER: 39,132
; REFERENCE/DOCKET NUMBER: PF-0513 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 855-0555
; TELEFAX: (650) 845-4166
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 252 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-09-071-709-10

Query Match 100.0%; Score 948; DB 4; Length 252;
Best Local Similarity 100.0%; Pred. No. 3.1e-92;
Matches 170; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ADERSIHDFCLVSKVGRASMPRWYNTDGSQCLFVYGGDGNNSNYLTKEECLKK 60
Db 28 ADERSIHDFCLVSKVGRASMPRWYNTDGSQCLFVYGGDGNNSNYLTKEECLKK 87
Qy 61 CATVTENATGDLATSRNAADSSVPSAPRRQDSEHSDMFNVEEYCTANAVTGPCRASFP 120
Db 88 CATVTENATGDLATSRNAADSSVPSAPRRQDSEHSDMFNVEEYCTANAVTGPCRASFP 147
Qy 121 RWFYDVERNSCNFIYGGCRGNKNSYRSEAEACMLRCFRQENPPLPLGSK 170
Db 148 RWFYDVERNSCNFIYGGCRGNKNSYRSEAEACMLRCFRQENPPLPLGSK 197

RESULT 4
US-09-013-896A-2
; Sequence 2, Application US/09013896A
; Patent No. 6262233
; GENERAL INFORMATION:
; APPLICANT: GENTZ, REINER
; TITLE OF INVENTION: TISSUE FACTOR PATHWAY INHIBITOR-3
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
; STREET: 1100 NEW YORK AVE., NW, STE. 600

CITY: WASHINGTON
STATE: DC
COUNTRY: US
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/013,896A
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: STEFFE, ERIC K.
REGISTRATION NUMBER: 36,688
REFERENCE/DOCKET NUMBER: 1488.1290001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
TELEFAX: (301) 309-8439
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 252 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-013-896A-2

Query Match 100.0%; Score 948; DB 4; Length 252;
Best Local Similarity 100.0%; Pred. No. 3.1e-92;
Matches 170; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ADERSIHDFCLVSKVVGRCRASPRWYNTDGSQOLFVYGGCDGNSNNYLTKEECLKK 60
Db 28 ADERSIHDFCLVSKVVGRCRASPRWYNTDGSQOLFVYGGCDGNSNNYLTKEECLKK 87
QY 61 CATVTENATGDLATSRNAADSSVPSAPRRQDSHSDMFNVEEYCTANAVTGPCRASFP 120
Db 88 CATVTENATGDLATSRNAADSSVPSAPRRQDSHSDMFNVEEYCTANAVTGPCRASFP 147
QY 121 RWYFDVERNSCNNFIYGGCGNKNYSRSEACMLRCFROQENPLPLGSK 170
Db 148 RWYFDVERNSCNNFIYGGCGNKNYSRSEACMLRCFROQENPLPLGSK 197

RESULT 5
US-08-685-558A-18
Sequence 18, Application US/08685558A
Patent No. 6225081
GENERAL INFORMATION:
APPLICANT: SHIMOMURA, Takeshi
APPLICANT: KAWAGUCHI, Toshiya
APPLICANT: KITAMURA, Naomi
APPLICANT: MIYAZAWA, Keiji
TITLE OF INVENTION: NOVEL PROTEIN, DNA CODING FOR SAME
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: SUGHRUE, MION, ZINN, MACPEAK & SEAS
STREET: 2100 Pennsylvania Avenue, N.W.
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20037
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/685,558A
FILING DATE: 24-JUL-1996
PRIOR APPLICATION DATA:

APPLICATION NUMBER: JPA Hei 7-187135
FILING DATE: 24-JUL-1995
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 513 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
STRAIN: MKN45
US-08-685-558A-18
Query Match 32.9%; Score 312; DB 4; Length 513;
Best Local Similarity 33.5%; Pred. No. 7.6e-25;
Matches 67; Conservative 24; Mismatches 71; Indels 38; Gaps 5;
QY 5 RSIHDFCLVSKVVGRCRASPRWYNTDGSQOLFVYGGCDGNSNNYLTKEECLKKCATV 64
Db 244 KOTEDYCLASNKVGRGSGSFPWYDPTQICKSFYVGGCLGNKNYLRREECILACRGV 303
QY 65 -----TENATGDLATSRNAADS-----SVPSAPRRQDS-----EDHSSDMFNY 102
Db 304 QGFSMERHHPVCSGTQPTQFRGSCGCCIDSLFLECDTTPNCPPDASDEAAACEKYTSGFDEL 363
QY 103 EE-----YCTANAVTGPCRASFPWYFDVERNSCNNFIYGGCGNKNYSRSEACML 154
Db 364 QRHFFSDKGHCVDLPTDGLCKESIPRWYINPFSEHCAREFTYGGCYGNKNNFEEQOOLE 423
QY 155 RC-----FRQENPLPLP 166
Db 424 SCRGISKDVFGLRREIP 443
RESULT 6
US-09-071-709-2
Sequence 2, Application US/09071709
Patent No. 6171790
GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer L.
APPLICANT: Tang, Y. Tom
APPLICANT: Lal, Preeti
APPLICANT: Corley, Neil C.
APPLICANT: Guegler, Karl J.
APPLICANT: Patterson, Chandra
TITLE OF INVENTION: HUMAN PROTEASE ASSOCIATED PROTEINS
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
STREET: 3174 PORTER DRIVE
CITY: PALO ALTO
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/071,709
FILING DATE: Filed Herewith
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: CERRONE, MICHAEL C.
REGISTRATION NUMBER: 39,132
REFERENCE/DOCKET NUMBER: PF-0513 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 855-0555
TELEFAX: (650) 845-4166
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:

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; LENGTH: 348 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: BLADNOT04
; CLONE: 1319265
; US-09-071-709-2

Query Match 31.6%; Score 299.5; DB 4; Length 348;
Best Local Similarity 31.2%; Pred. No. 9.6e-24;
Matches 69; Conservative 24; Mismatches 65; Indels 63; Gaps 7;

QY 5 RSTHDFCLSVKVVGV-RCRASMPRWYNTDGSQCLFYVGGCGNSNNYLTKECLKKCAT 63
Db 62 KQTEYCLASNKKVRCRGSPRWYDPTFQICKSFYVGGCLGNKNYLRREECILACRG 121
QY 64 VTNATGDLATSRNAADSSVPSAP---RRQ-----DSED-- 94
Db 122 V----GGPLRGSSGAATPQPGSMERRHPVCSGTQPTQFRCSNGCCIDSPLECDTTP 177
QY 95 ---HSSDMFNVEY-----CTANAVTGPCRASFPRWYFDVERNSCNN 133
Db 178 NCPDASDEAAACEKYSFGDELQRIHPFSDKGHCVDLPDTGLCKRESTPRWYINPFSEHCAR 237
QY 134 FIYGGCGNKNKNSRSEACMLRC-----FRQENPPPLP 166
Db 238 FTYGGCYGNKNNEEQCLCSRGISKKDVFGLRREIPI 278

RESULT 7
US-09-013-896A-10
; Sequence 10, Application US/09013896A
; Patent No. 6262233
; GENERAL INFORMATION:
; APPLICANT: GENTZ, REINER
; TITLE OF INVENTION: TISSUE FACTOR PATHWAY INHIBITOR-3
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
; STREET: 1100 NEW YORK AVE., NW, STE. 600
; CITY: WASHINGTON
; STATE: DC
; COUNTRY: US
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/013,896A
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: STEFFE, ERIC K.
; REGISTRATION NUMBER: 36,688
; REFERENCE/DOCKET NUMBER: 1488.1290001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 309-8504
; TELEFAX: (301) 309-8439
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 51 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-013-896A-10

Query Match 31.3%; Score 297; DB 4; Length 51;
Best Local Similarity 100.0%; Pred. No. 1.5e-24;
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 106 CTANAVTGPCRASFPRWYFDVERNSCNNFIYGGCGNKNKNSRSEACMLRC 156
Db 1 CTANAVTGPCRASFPRWYFDVERNSCNNFIYGGCGNKNKNSRSEACMLRC 51

RESULT 9
US-08-422-333-12
; Sequence 12, Application US/08422333
; Patent No. 5912410
; GENERAL INFORMATION:
; APPLICANT: CORDELL, Barbara L.
; TITLE OF INVENTION: TRANSGENIC NON-HUMAN MAMMAL DISPLAYING
; THE AMYLOID-FORMING PATHOLOGY OF ALZHEIMER'S DISEASE
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Scios, Inc.
; STREET: 2450 Bayshore Parkway
; CITY: Mountain View
; STATE: CA
; COUNTRY: USA
; ZIP: 94043
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
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; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/422,333
; FILING DATE: 13-APR-1995
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Shearer, Peter R.
; REGISTRATION NUMBER: 28,117
; REFERENCE/DOCKET NUMBER: 21900-28048.00
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 966-1550
; TELEFAX: (415) 966-2438
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 122 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-422-333-12

Query Match 26.1%; Score 247.5; DB 2; Length 122;
Best Local Similarity 32.4%; Pred. No. 7.5e-19;
Matches 48; Conservative 16; Mismatches 45; Indels 39; Gaps 1;

QY 9 DFCLSVKVGRCRASPRWYNTDGSQCLFVYGGDGNNSNYLTKEECLKKCATVTENA 68
Db 3 DSCOLDYSQGPCLGFLKFRFYNGTSMACETFLYGGCMGNLNNFLSKQECLOTCTV--- 58

QY 69 TGLATSRNAADSSVPSAPRRQDSEHSDMFNYEYCTANAVTGPCRASFFRWYFDVER 128
Db 59 -----EACNLPIVQGPCRAFIQLWAFDAVK 83

QY 129 NSCNNFIYGGRCGNKNSYRSEACMLRC 156
Db 84 GKCVRFSGGCKGNKNGKFSQKEKEYC 111

Query Match 26.1%; Score 247.5; DB 6; Length 122;
Best Local Similarity 32.4%; Pred. No. 7.5e-19;
Matches 48; Conservative 16; Mismatches 45; Indels 39; Gaps 1;

QY 9 DFCLSVKVGRCRASPRWYNTDGSQCLFVYGGDGNNSNYLTKEECLKKCATVTENA 68
Db 3 DSCOLDYSQGPCLGFLKFRFYNGTSMACETFLYGGCMGNLNNFLSKQECLOTCTV--- 58

QY 69 TGLATSRNAADSSVPSAPRRQDSEHSDMFNYEYCTANAVTGPCRASFFRWYFDVER 128
Db 59 -----EACNLPIVQGPCRAFIQLWAFDAVK 83

QY 129 NSCNNFIYGGRCGNKNSYRSEACMLRC 156
Db 84 GKCVRFSGGCKGNKNGKFSQKEKEYC 111

RESULT 10
5187153-20
; Patent No. 5187153
; APPLICANT: CORDELL, BARBARA; SCHILLING, JAMES W.; KATUNUMA, NOBUHIKO
; TITLE OF INVENTION: METHODS OF TREATMENT USING ALZHEIMER'S
; AMYLOID POLYPEPTIDE DERIVATIVES
; NUMBER OF SEQUENCES: 33
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/502,273
; FILING DATE: 29-MAR-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 361,912
; FILING DATE: 06-JUN-1989
; APPLICATION NUMBER: 359,911
; FILING DATE: 12-MAY-1989
; APPLICATION NUMBER: 87,002
; FILING DATE: 18-AUG-1987
; APPLICATION NUMBER: 8,810
; FILING DATE: 30-JAN-1987
; APPLICATION NUMBER: 948,376
; FILING DATE: 31-DEC-1986
; APPLICATION NUMBER: 932,193
; FILING DATE: 17-NOV-1986
; SEQ ID NO: 20:
; LENGTH: 122
5187153-20

Query Match 26.1%; Score 247.5; DB 6; Length 122;
Best Local Similarity 32.4%; Pred. No. 7.5e-19;
Matches 48; Conservative 16; Mismatches 45; Indels 39; Gaps 1;

QY 9 DFCLSVKVGRCRASPRWYNTDGSQCLFVYGGDGNNSNYLTKEECLKKCATVTENA 68
Db 3 DSCOLDYSQGPCLGFLKFRFYNGTSMACETFLYGGCMGNLNNFLSKQECLOTCTV--- 58

QY 69 TGLATSRNAADSSVPSAPRRQDSEHSDMFNYEYCTANAVTGPCRASFFRWYFDVER 128
Db 59 -----EACNLPIVQGPCRAFIQLWAFDAVK 83

QY 129 NSCNNFIYGGRCGNKNSYRSEACMLRC 156
Db 84 GKCVRFSGGCKGNKNGKFSQKEKEYC 111

RESULT 12
US-08-422-333-10
; Sequence 10, Application US/08/422333
; Patent No. 5912410
; GENERAL INFORMATION:
; APPLICANT: CORDELL, Barbara L.
; TITLE OF INVENTION: TRANSGENIC NON-HUMAN MAMMAL DISPLAYING
; TITLE OF INVENTION: THE AMYLOID-FORMING PATHOLOGY OF ALZHEIMER'S DISEASE
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Scios, Inc.
; STREET: 2450 Bayshore Parkway
; CITY: Mountain View
; STATE: CA
; COUNTRY: USA
; ZIP: 94043
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/422,333

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QY 69 TGLATSRNAADSSVPSAPRRQDSEHSDMFNYEYCTANAVTGPCRASFFRWYFDVER 128
Db 59 -----EACNLPIVQGPCRAFIQLWAFDAVK 83

QY 129 NSCNNFIYGGRCGNKNSYRSEACMLRC 156
Db 84 GKCVRFSGGCKGNKNGKFSQKEKEYC 111

RESULT 11
5220013-23
; Patent No. 5220013
; APPLICANT: PONTE, PHYLLIS A.; CORDELL, BARBARA
; TITLE OF INVENTION: DNA SEQUENCE USEFUL FOR THE DETECTION
; OF ALZHEIMER'S DISEASE
; NUMBER OF SEQUENCES: 30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/444,118
; FILING DATE: 30-NOV-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 87,002
; FILING DATE: 18-AUG-1987
; APPLICATION NUMBER: 8,810
; FILING DATE: 30-JAN-1987
; APPLICATION NUMBER: 948,376
; FILING DATE: 31-DEC-1986
; APPLICATION NUMBER: 932,193
; FILING DATE: 17-NOV-1986
; SEQ ID NO: 23:
; LENGTH: 122
5220013-23
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Query Match 26.1%; Score 247.5; DB 6; Length 122;
Best Local Similarity 32.4%; Pred. No. 7.5e-19;
Matches 48; Conservative 16; Mismatches 45; Indels 39; Gaps 1;

QY 9 DFCLSVKVGRCRASPRWYNTDGSQCLFVYGGDGNNSNYLTKEECLKKCATVTENA 68
Db 3 DSCOLDYSQGPCLGFLKFRFYNGTSMACETFLYGGCMGNLNNFLSKQECLOTCTV--- 58

QY 69 TGLATSRNAADSSVPSAPRRQDSEHSDMFNYEYCTANAVTGPCRASFFRWYFDVER 128
Db 59 -----EACNLPIVQGPCRAFIQLWAFDAVK 83

QY 129 NSCNNFIYGGRCGNKNSYRSEACMLRC 156
Db 84 GKCVRFSGGCKGNKNGKFSQKEKEYC 111

RESULT 12
US-08-422-333-10
; Sequence 10, Application US/08/422333
; Patent No. 5912410
; GENERAL INFORMATION:
; APPLICANT: CORDELL, Barbara L.
; TITLE OF INVENTION: TRANSGENIC NON-HUMAN MAMMAL DISPLAYING
; TITLE OF INVENTION: THE AMYLOID-FORMING PATHOLOGY OF ALZHEIMER'S DISEASE
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Scios, Inc.
; STREET: 2450 Bayshore Parkway
; CITY: Mountain View
; STATE: CA
; COUNTRY: USA
; ZIP: 94043
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/422,333

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Fri Oct 18 10:50:22 2002

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; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/358,160
; FILING DATE: 16-DEC-1994
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/133,031
; FILING DATE: 13-OCT-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/009,319
; FILING DATE: 26-JAN-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/664,989
; FILING DATE: 01-MAR-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/487,063
; FILING DATE: 02-MAR-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/240,160
; FILING DATE: 02-SEP-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Cooper, Iver P.
; REGISTRATION NUMBER: 28,005
; REFERENCE/DOCKET NUMBER: LEY-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; TELEX: 248633
; INFORMATION FOR SEQ ID NO: 72:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 147 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-358-160-72

Query Match 25.8%; Score 244.5; DB 1; Length 147;
Best Local Similarity 32.4%; Pred. No. 2e-18;
Matches 48; Conservative 14; Mismatches 47; Indels 39; Gaps 1;

QY 9 DFCLVSKVYGRCRASMPRWYNYVTDGSCQLFYVYGGDGNNSNYLTKECLKKCATVTENA 68
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
24 DSCOLGYSAGPCMGMTSRFYNGTSMACETFYGGCMGNNGNNFVTEKECLQTCRTVAA-- 81

QY 69 TGDLATSRNAADSSVPSAPRRQSDSDHSSDMFNVEYCTANAVTGPCRASFPWYFDVER 128
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
82 -----CNLPYVRGPCRAFIQLWAFDAVK 104

QY 129 NSCNNFYGGCRGNKNSYRSEECMLRC 156
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
105 GKCVLFYGGCGQGNKNFYSEKECREYC 132

Search completed: October 18, 2002, 10:36:06
Job time : 15 secs
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GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: October 18, 2002, 10:33:48 ; Search time 28 seconds
(without alignments)
1050.326 Million cell updates/sec

Title: US-09-218-913d-52

Perfect score: 948

Sequence: 1 ADERSIHDFCLVSKVGRG.....ACMLRCFRQENPPLGLSK 170

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 562222 seqs, 172994929 residues

Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- 1: sp_archaea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_mhc:*
- 8: sp_organelle:*
- 9: sp_phase:*
- 10: sp_plant:*
- 11: sp_rodent:*
- 12: sp_virus:*
- 13: sp_vertebrate:*
- 14: sp_unclassified:*
- 15: sp_rvirus:*
- 16: sp_bacteriap:*
- 17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	948	100.0	252	4	Q969E0 homo sapien
2	381	40.2	195	11	Q9D808
3	294	31.0	507	11	Q9D3K4
4	294	31.0	507	11	Q99J04
5	259	27.3	3060	5	Q9VAV4
6	256.5	27.1	1572	5	O44938
7	255	26.9	3198	5	Q9U8G8
8	252	26.6	287	13	Q93424
9	250.5	26.4	2167	5	O76840
10	250	26.4	2174	5	Q9GQ90
11	244.5	25.8	151	4	P78491
12	240	25.3	2225	5	O45881
13	239.5	25.3	396	6	O28874
14	235.5	24.8	349	11	Q9DBU9
15	235.5	24.8	349	11	Q925W1
16	233.5	24.6	352	11	O70160

17	228	24.1	251	4	O95103	O95103 homo sapien
18	227.5	24.0	246	11	Q9Z208	Q9Z208 mus musculus
19	222	23.4	1043	5	O17644	O17644 caenorhabdi
20	219.5	23.2	342	13	P70004	P70004 xenopus lae
21	219	23.1	922	5	Q21418	Q21418 caenorhabdi
22	209	22.0	1743	5	Q9XWXS	Q9XWXS caenorhabdi
23	208	21.9	751	11	Q60709	Q60709 mus musculus
24	208	21.9	763	11	O61482	O61482 mus musculus
25	200	21.1	523	4	O14594	O14594 homo sapien
26	200	21.1	1599	5	Q09983	Q09983 caenorhabdi
27	199	21.0	1522	5	Q22685	Q22685 caenorhabdi
28	198	20.9	1195	5	Q9N343	Q9N343 caenorhabdi
29	195	20.6	1391	5	O19021	O19021 caenorhabdi
30	194	20.5	1297	5	Q9U350	Q9U350 caenorhabdi
31	193	20.4	1474	5	O62504	O62504 caenorhabdi
32	192	20.3	491	4	Q9S820	Q9S820 homo sapien
33	192	20.3	548	4	Q96N28	Q96N28 homo sapien
34	188	19.8	751	13	Q9DGJ7	Q9DGJ7 gallus gall
35	186.5	19.7	747	13	Q91963	Q91963 xenopus. ap
36	186.5	19.7	984	5	Q9GQ2	Q9GQ2 calliactis
37	186.5	19.7	984	5	Q9GQ1	Q9GQ1 calliactis
38	186	19.6	484	4	O13793	O13793 homo sapien
39	186	19.6	547	4	O13764	O13764 homo sapien
40	186	19.6	770	6	Q9TUI0	Q9TUI0 sus scrofa
41	185.5	19.6	1203	5	O45916	O45916 caenorhabdi
42	183.5	19.4	607	11	Q99K32	Q99K32 mus musculus
43	183	19.3	160	11	Q9QZ78	Q9QZ78 cavia sp. p
44	178	18.8	1965	5	O61893	O61893 caenorhabdi
45	177	18.7	59	5	Q9TWF8	Q9TWF8 anemonia su

ALIGNMENTS

RESULT 1

Q969E0	PRELIMINARY;	PRT;	252 AA.
ID	Q969E0		
AC	Q969E0;		
DT	01-DEC-2001 (TREMBLrel. 19, Created)		
DT	01-DEC-2001 (TREMBLrel. 19, Last sequence update)		
DT	01-DEC-2001 (TREMBLrel. 19, Last annotation update)		
DE	SERINE PROTEASE INHIBITOR, KUNITZ TYPE, 2.		
OS	Homo sapiens (Human).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
OX	NCBI_TaxID=9606;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	TISSUE=OVARY, AND ADENOCARCINOMA;		
RA	Strausberg R.;		
RL	Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.		
RN	[2]		
RP	SEQUENCE FROM N.A.		
RC	TISSUE=OVARY, AND ADENOCARCINOMA;		
RA	Strausberg R.;		
RL	Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.		
RN	[3]		
RP	SEQUENCE FROM N.A.		
RC	TISSUE=OVARY, AND ADENOCARCINOMA;		
RA	Strausberg R.;		
RL	Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.		
DR	EMBL; BC012868; AAH12868.1; -		
DR	EMBL; BC007705; AAH07705.1; -		
DR	EMBL; BC011951; AAH11951.1; -		
DR	EMBL; BC011955; AAH11955.1; -		
KW	Protease.		
SQ	SEQUENCE 252 AA; 28242 MW; FDD3360C1E3A7057 CRC64;		

Query Match 100.0%; Score 948; DB 4; Length 252;

Best Local Similarity 100.0%; Pred. No. 8.3e-93;

Matches 170; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADERSIHDFCLVSKVGRG.....ACMLRCFRQENPPLGLSK 170

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28 ADERSHDFCLVSKVGRCRASMPRWNVTDGSQLFVYGGCGNSNNYLTKECLKK 87
QY 61 CATVTENATGDLATSNADSSVPSAPRQDSEHSDMFNEEYCTANAVTGPCRASFP 120
|||||
Db 88 CATVTENATGDLATSNADSSVPSAPRQDSEHSDMFNEEYCTANAVTGPCRASFP 147
|||||
QY 121 RWYFDVERNSCNNFIYGGCRGNKNSYRSEACMLRCFROQENPPLPLGSK 170
|||||
Db 148 RWYFDVERNSCNNFIYGGCRGNKNSYRSEACMLRCFROQENPPLPLGSK 197
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RESULT 2
Q9D808 PRELIMINARY; PRT; 195 AA.
AC Q9D808:
DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE SERINE PROTEASE INHIBITOR, KUNITZ TYPE 2.
GN SPINT2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=PANCREAS;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleschmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaide I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Sakamoto N.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Willing L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA Hayashizaki Y.,
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
DR EMBL; AK017342; BAB30697.1; -.
DR HSSP; P05067; 1CA0.
DR MGD; MGI:1338033; Spint1.
DR InterPro; IPR002223; Kunitz_BPTI.
DR InterPro; IPR002172; LDL_recept_A.
DR Pfam; PF00014; Kunitz_BPTI; 2.
DR Pfam; PF00057; ldl_recept_a; 1.
DR PRINTS; PR00759; BASICPTASE.
DR SMART; SM00131; KU; 2.
DR SMART; SM00192; LDLa; 1.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR PROSITE; PS00279; BPTI_KUNITZ_2; 2.
DR PROSITE; PS00068; LDLRA_2; 1.
KW Glycoprotein; Serine protease inhibitor.
SQ SEQUENCE 195 AA; 21705 MW; 1ABD78CEFF175DE1 CRC64;

Query Match 40.2%; Score 381; DB 11; Length 195;
Best Local Similarity 64.5%; Pred. No. 1.1e-32;
Matches 69; Conservative 14; Mismatches 24; Indels 0; Gaps 0;

QY 64 VTENATGDLATSNADSSVPSAPRQDSEHSDMFNEEYCTANAVTGPCRASFP 123
|||||
Db 34 VHTNTDDMARNRGADSVSLVPSRQSAEDLSAEIFNEEYCVKVPKRAAPRWY 93
|||||
QY 124 FVERNSCNNFIYGGCRGNKNSYRSEACMLRCFROQENPPLPLGSK 170
|||||
Db 94 YDEKNSCISFIYGGCRGNKNSYLSOEAQHCSGKQMPFLTPGLK 140
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RESULT 3
Q9D3K4 PRELIMINARY; PRT; 507 AA.
AC Q9D3K4:
DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE SERINE PROTEASE INHIBITOR, KUNITZ TYPE 1.
GN SPINT1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=HEAD;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleschmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaide I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Sakamoto N.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Willing L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA Hayashizaki Y.,
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
DR EMBL; AK017342; BAB30697.1; -.
DR HSSP; P05067; 1CA0.
DR MGD; MGI:1338033; Spint1.
DR InterPro; IPR002223; Kunitz_BPTI.
DR InterPro; IPR002172; LDL_recept_A.
DR Pfam; PF00014; Kunitz_BPTI; 2.
DR Pfam; PF00057; ldl_recept_a; 1.
DR PRINTS; PR00759; BASICPTASE.
DR SMART; SM00131; KU; 2.
DR SMART; SM00192; LDLa; 1.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR PROSITE; PS00279; BPTI_KUNITZ_2; 2.
DR PROSITE; PS00068; LDLRA_2; 1.
KW Glycoprotein; Serine protease inhibitor.
SQ SEQUENCE 507 AA; 56571 MW; 9E0A29B7056D72D CRC64;

Query Match 31.0%; Score 294; DB 11; Length 507;
Best Local Similarity 32.4%; Pred. No. 5.8e-23;
Matches 59; Conservative 23; Mismatches 70; Indels 30; Gaps 3;

QY 5 RSHDFCLVSKVGRCRASMPRWNVTDGSQLFVYGGCGNSNNYLTKECLKKCATV 64
|||||
Db 238 KOTEDYCLASYKVGRCGSPRMYDPRKQICKSFTEGCLGNKNYLRREECMLACKDV 297
|||||
QY 65 -----TENATGDLATSNAD-----SSVPSAPRQDSEHSDMFNEE- 104
|||||
Db 298 QGISPKRHHFVCSGSHATQFRCSNCCIDGFLCEDDTPDCPDGSEATCEKYSGFDEL 357
|||||
QY 105 -----YCTANAVTGPCRASFPYFDVERNSCNNFIYGGCRGNKNSYRSEACML 154
|||||
Db 358 QNIHFLSDGYCAELPDTGTCKENIPRWYNPFSERCARFTYGGCYGNKNFEEQOCLE 417
|||||
QY 155 RC 156
Db 418 SC 419

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RC	STRAIN=BERKELEY;	PRT;	507 AA.
RA	MEDLINE=20196006; PubMed=10731132;		
RA	Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,		
RA	Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,		
RA	George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,		
RA	Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,		
RA	Brandon R.C., Rogers Y.H.C., Blazej R.G., Champe M., Pfeiffer B.D.,		
RA	Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.B.G.,		
RA	Abriel J.F., Agbayani A., An H.-J., Andrews-Pfannkuch C., Baldwin D.,		
RA	Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,		
RA	Beeson K.V., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,		
RA	Borkova D., Butchan M.R., Bouck J., Brokstein P., Brottier P.,		
RA	Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,		
RA	Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,		
RA	de Pablo J.B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,		
RA	Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,		
RA	Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,		
RA	Fosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,		
RA	Glocke A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,		
RA	Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,		
RA	Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,		
RA	Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,		
RA	Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,		
RA	Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,		
RA	Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,		
RA	Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,		
RA	Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,		
RA	Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,		
RA	Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,		
RA	Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,		
RA	Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,		
RA	Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,		
RA	Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,		
RA	Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weissbach J.,		
RA	Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,		
RA	Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,		
RA	Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,		
RA	Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;		
RT	"The genome sequence of Drosophila melanogaster.";		
RL	Science 287:2185-2195(2000).		
CC	-1- ALTERNATIVE PRODUCTS: 2 ISOFORMS: A LONG FORM (SHOWN HERE) AND A		
DR	SHORT FORM; ARE PRODUCED BY ALTERNATIVE SPLICING.		
DR	EMBL; AE003765; AAF56794.2; -		
DR	HSSP; P12111; 2KNT.		
DR	FlyBase: FBgn0003137; Ppn.		
DR	InterPro; IPR000561; EGF-like.		
DR	InterPro; IPR003598; Ig_c2.		
DR	InterPro; IPR003006; Ig_MHC.		
DR	InterPro; IPR002223; Kunitz_BPTI.		
DR	InterPro; IPR000884; TSPI.		
DR	InterPro; IPR002221; WAP.		
DR	Pfam; PF00047; ig_3.		
DR	Pfam; PF00014; Kunitz_BPTI; 12.		
DR	Pfam; PF00090; tsp_1; 5.		
DR	Pfam; PF00095; wap; 1.		
DR	PRINTS; PR00759; BASICPTASE.		
DR	SMART; SM00408; IGC2; 3.		
DR	SMART; SM00131; KU; 12.		
DR	SMART; SM00209; TSPI; 7.		
DR	SMART; SM00217; WAP; 1.		
DR	PROSITE; PS00317; 4-DISULFIDE_CORE; 1.		
DR	PROSITE; PS00280; BPTI_KUNITZ_1; 11.		
DR	PROSITE; PS00279; BPTI_KUNITZ_2; 12.		
DR	PROSITE; PS00022; EGF_1; UNKNOWN_1.		
DR	PROSITE; PS00092; TSPI; 3.		
DR	Alternative splicing; Immunoglobulin domain;		
KW	Serine protease inhibitor.		
FT	VARSPLIC 2803 2803		
FT	VARSPLIC 2844 2854		
FT	VARSPLIC 2855 3060		
FT	SEQUENCE 3060 AA; 331579 MW; ACA31D3BE558C7C0 CRC64;		
SO	SEQUENCE FROM N.A.		

RC	STRAIN=BERKELEY;	PRT;	507 AA.
RA	MEDLINE=20196006; PubMed=10731132;		
RA	Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,		
RA	Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,		
RA	George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,		
RA	Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,		
RA	Brandon R.C., Rogers Y.H.C., Blazej R.G., Champe M., Pfeiffer B.D.,		
RA	Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.B.G.,		
RA	Abriel J.F., Agbayani A., An H.-J., Andrews-Pfannkuch C., Baldwin D.,		
RA	Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,		
RA	Beeson K.V., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,		
RA	Borkova D., Butchan M.R., Bouck J., Brokstein P., Brottier P.,		
RA	Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,		
RA	Cherry J.M., Cawley S., Dahike C., Davenport L.B., Davies P.,		
RA	de Pablo J.B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,		
RA	Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,		
RA	Durbin K.J., Evangelista C.C., Ferraz C., Ferrera S., Fleischmann W.,		
RA	Foster C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,		
RA	Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,		
RA	Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,		
RA	Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,		
RA	Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,		
RA	Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,		
RA	Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,		
RA	Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,		
RA	Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,		
RA	Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,		
RA	Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,		
RA	Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,		
RA	Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,		
RA	Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,		
RA	Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,		
RA	Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,		
RA	Wang Z.-Y., Wassarman D.A., Weinstein G.M., Weissbach J.,		
RA	Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,		
RA	Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,		
RA	Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,		
RT	Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;		
RT	"The genome sequence of Drosophila melanogaster.";		
RL	Science 287:2185-2195(2000).		
CC	-1- ALTERNATIVE PRODUCTS: 2 ISOFORMS: A LONG FORM (SHOWN HERE) AND A		
CC	SHORT FORM; ARE PRODUCED BY ALTERNATIVE SPLICING.		
DR	EMBL; AE003765; AAF56794.2; -		
DR	EMBL; AE003765; AAF56795.2; -		
DR	HSSP; P12111; 2KNT.		
DR	FlyBase: FBgn0003137; Ppn.		
DR	InterPro; IPR000561; EGF-like.		
DR	InterPro; IPR003598; Ig_c2.		
DR	InterPro; IPR003006; Ig_MHC.		
DR	InterPro; IPR002223; Kunitz_BPTI.		
DR	InterPro; IPR000884; TSPI.		
DR	InterPro; IPR002221; WAP.		
DR	Pfam; PF00047; ig_3.		
DR	Pfam; PF00014; Kunitz_BPTI; 12.		
DR	Pfam; PF00090; tsp_1; 5.		
DR	Pfam; PF00095; wap; 1.		
DR	PRINTS; PR00759; BASICPTASE.		
DR	SMART; SM00408; IGC2; 3.		
DR	SMART; SM00131; KU; 12.		
DR	SMART; SM00209; TSPI; 7.		
DR	SMART; SM00217; WAP; 1.		
DR	PROSITE; PS00317; 4-DISULFIDE_CORE; 1.		
DR	PROSITE; PS00280; BPTI_KUNITZ_1; 11.		
DR	PROSITE; PS00279; BPTI_KUNITZ_2; 12.		
DR	PROSITE; PS00022; EGF_1; UNKNOWN_1.		
DR	PROSITE; PS00092; TSPI; 3.		
KW	Alternative splicing; Immunoglobulin domain;		
KW	Serine protease inhibitor.		
FT	VARSPLIC 2803 2803		
FT	VARSPLIC 2844 2854		
FT	VARSPLIC 2855 3060		
FT	SEQUENCE 3060 AA; 331579 MW; ACA31D3BE558C7C0 CRC64;		
FT	MISSING (IN SHORT ISOFORM).		
FT	ENFKTMSDGI -> VASPLIPNAV (IN SHORT ISOFORM).		
FT	ISOFORM.		
FT	VARSPPLIC 2844 2854		
FT	VARSPPLIC 2855 3060		
FT	SEQUENCE 3060 AA; 331579 MW; ACA31D3BE558C7C0 CRC64;		
FT	MISSING (IN SHORT ISOFORM).		
FT	VARSPPLIC 2844 2854		
FT	VARSPPLIC 2855 3060		
FT	SEQUENCE 3060 AA; 331579 MW; ACA31D3BE558C7C0 CRC64;		
FT	MISSING (IN SHORT ISOFORM).		

ID	Q9U8G8	PRELIMINARY;	PRT;	3198 AA.
AC	Q9U8G8;			
DT	01-MAY-2000 (TrEMBLrel. 13, Created)			
DT	01-MAY-2000 (TrEMBLrel. 13, Last sequence update)			
DT	01-DEC-2001 (TrEMBLrel. 19, Last annotation update)			
DE	LACUNIN PRECURSOR.			
OS	Manduca sexta (Tobacco hawkmoth) (Tobacco hornworm).			
OC	Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;			
OC	Pterygota; Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;			
OC	Sphingodea; Sphingidae; Sphinginae; Manduca.			
OX	NCBI_TaxID=7130;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=99457716; PubMed=10528409;			
RA	Nardi J.B., Martos R., Walden K.K., Lampe D.J., Robertson H.M.;			
RT	"Expression of lacunin, a large multidomain extracellular matrix			
RT	protein, accompanies morphogenesis of epithelial monolayers in Manduca			
RT	sexta.";			
RL	Insect Biochem. Mol. Biol. 29:883-897(1999).			
DR	EMBL; AF078161; AAF04457.1; -.			
DR	HSP; P12111; 2KNT.			
DR	InterPro; IPR004094; Antistasin.			
DR	InterPro; IPR003598; Ig_C2.			
DR	InterPro; IPR003006; Ig_MHC.			
DR	InterPro; IPR002223; Kunitz_BPTI.			
DR	InterPro; IPR000884; TSPI.			
DR	InterPro; IPR002221; WAP.			
DR	Pfam; PF02822; Antistasin; 4.			
DR	Pfam; PF00047; ig; 2.			
DR	Pfam; PF00014; Kunitz_BPTI; 9.			
DR	Pfam; PF00095; wap; 1.			
DR	PRINTS; PR00759; BASICPTASE.			
DR	SMART; SM00408; IGC2; 2.			
DR	SMART; SM00131; KU; 10.			
DR	SMART; SM00209; TSPI; 7.			
DR	SMART; SM00217; WAP; 1.			
DR	PROSITE; PS00317; 4_DISULFIDE_CORE; 1.			
DR	PROSITE; PS00280; BPTI_KUNITZ_1; 8.			
DR	PROSITE; PS00279; BPTI_KUNITZ_2; 10.			
DR	PROSITE; PS50092; TSPI; 1.			
KW	Immunoglobulin domain; Serine protease inhibitor; Signal.			
FT	SIGNAL 1 21 POTENTIAL.			
SQ	SEQUENCE 3198 AA; 349364 MW; ABACDA59CD09134 CRC64;			
Query Match 26.9%; Score 255; DB 5; Length 3198;				
Best Local Similarity 31.7%; Pred. No. 6.9e-18;				
Matches 51; Conservative 23; Mismatches 63; Indels 24; Gaps				
Qy	9 DFCLSVKVVGRCRASPRWYNTDGSOLFVYGCDGNSNNYLTKECLKCATVTENA 68			
Db	2133 DLCLTPAAIGDCAVDREYRWDYTRKSCQFYFGCGAGNFNATQAECEGR----- 2185			
Qy	69 TGDLATSRNAADSSVPSAPRODSDHSDMFNFEYCYTANAVTGPCRASPRWYFDVER 128			
Db	2186 -----SEAKITTVR--PTEAHP-----LTEMCFMEKDPGCTDTETRWVYDKL 2228			
Qy	129 NSCNFFIYGCGRGNKNYSREACMLRCFRQENPLPLGS 169			
Db	2229 GKCVTFEYGCGRNRRNFTTEEYCYCGTAGDQLCLPMS 2269			
RESULT 8				
O93424	PRELIMINARY;			
ID	Q93424			
AC	O93424;			
DT	01-NOV-1998 (TrEMBLrel. 08, Created)			
DT	01-NOV-1998 (TrEMBLrel. 08, Last sequence update)			
DT	01-DEC-2001 (TrEMBLrel. 19, Last annotation update)			
DE	HYPOPHETICAL 33.1 KDA PROTEIN.			
OS	Cyprinus carpio (Common carp).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;			

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OC Cypriniformes; Cyprinidae; Cyprinus.
OX NCBI_TaxID=7962;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=LIVER;
RA Gracey A.Y.;
RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF008648; AAC19410.1; -
DR HSSP; P31713; LSHP.
DR InterPro; IPR002223; Kunitz_BPTI.
DR Pfam; PF00014; Kunitz_BPTI; 3.
DR PRINTS; PR00759; BASICPTASE.
DR SMART; SM00131; KU; 3.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 3.
DR PROSITE; PS0279; BPTI_KUNITZ_2; 3.
KW Hypothetical protein; Serine protease inhibitor.
SQ SEQUENCE 287 AA; 33093 MW; DF69B3D76718115E CRC64;

Query Match 26.6%; Score 252; DB 13; Length 287;
Best Local Similarity 30.9%; Pred. No. 8.8e-19;
Matches 50; Conservative 19; Mismatches 53; Indels 40; Gaps 3;

QY 8 HDCLVSKVVGRCRASPWWYNTDGSQCLFYVGGCGNSNNYLKKECLKKCATVTEN 67
DB 39 HHSCKALKDEGCKALKDRFYDTDTGRGESFYGGCGQNNENFETLQCEKMCILV---- 94
QY 68 ATGDLATSRNADSSVPSAPRRDSEHSDMFNVEYCTANAVTGPCRASFPRWYFDVE 127
DB 95 -----KEDKSP-----COLDDEPGCGLVPRYFDFK 122
QY 128 RNSCNFFIYGGCGRNKNSRSEACMLRCF-----RQENPPL 165
DB 123 SQECKRFYGGCGFNGNFKTIKECHERCLPALNNMERNAPL 164

RESULT 9
O76840 PRELIMINARY; PRT; 2167 AA.
AC O76840; Q22911;
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE C37C3.6 PROTEIN.
GN C37C3.6.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Beloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BRISTOL N2;
RA Geisel C., Bradshaw H.;
RL "The sequence of C. elegans cosmid C37C3.";
RL Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.
CC -!- ALTERNATIVE PRODUCTS: TWO FORMS (A AND B) MAY BE PRODUCED BY
CC OF FORM B.
CC
DR EMBL; U64857; AAC25868.1; -.
DR EMBL; U64857; AAC25867.1; -.
DR HSSP; P00981; LDTK.
DR InterPro; IPR003598; Ig_c2.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR002223; Kunitz_BPTI.
DR InterPro; IPR000884; TSPI.
DR Pfam; PF00047; Ig; 1.
DR Pfam; PF00014; Kunitz_BPTI; 11.
DR Pfam; PF00090; tsp-1; 6.
DR PRINTS; PR00759; BASICPTASE.
DR SMART; SM00408; IGC2; 1.
DR SMART; SM00131; KU; 11.
DR SMART; SM00209; TSPI; 7.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 10.
DR PROSITE; PS0279; BPTI_KUNITZ_2; 11.
DR
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DR PROSITE; PS50092; TSPI; 4.
KW Alternative splicing; Hypothetical protein; Immunoglobulin domain;
KW Serine protease inhibitor.
FT VARSPLIC 147 155 MISSING (IN ISOFORM A).
FT VARSPLIC 1556 1558 KDD -> SKF (IN ISOFORM A).
FT VARSPLIC 1559 2167 MISSING (IN ISOFORM A).
SQ SEQUENCE 2167 AA; 237599 MW; 96274786D52E3639 CRC64;

Query Match 26.4%; Score 250.5; DB 5; Length 2167;
Best Local Similarity 30.1%; Pred. No. 1.3e-17;
Matches 49; Conservative 26; Mismatches 79; Indels 9; Gaps 1;

QY 5 RSIHDFCLVSKVVGRCRASPWWYNTDGSQCLFYVGGCGNSNNYLKKECLKKC--- 61
DB 1265 QSMEDICRSRQDAGPCETYSQWYNAFSECEFTFYGGCGNLNRRFSKDECEQRCFFV 1324
QY 62 -----ATVTENATGDLATSRNADSSVPSAPRRDSEHSDMFNVEEYCTANAVTGPC 115
DB 1325 HGAQPSAARQEQAPAAQAPQAPNSIVSPPOOSAPVVVPSNSKORDACHLNVDOGRC 1384
QY 116 RASFPRWYFDVERNSCNFFIYGGCGRNKNSRSEACMLRCFR 158
DB 1385 KGAFDSWYIEVATGSCVTKYTCGCGNANRFASKDOCESLCKV 1427

RESULT 10
Q9GQR0 PRELIMINARY; PRT; 2174 AA.
AC Q9GQR0;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE EXTRACELLULAR MATRIX PROTEIN PAPILIN PRECURSOR.
GN PPN.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=DP CN BW;
RX MEDLINE=20530499; PubMed=11076767;
RA Kramerova I.A., Kawaguchi N., Nelson R.E., Fessler L.I., Chen Y.,
RA Kramerov A.A., Kusche-Gullberg M., Kramer J.M., Ackley B.D.,
RA Sieron A.L., Prockop D.J., Fessler J.H.;
RT "Papilin in development; a pericellular protein with a homology to the
RT ADAMTS metalloproteinases.";
RL Development 127:5475-5485(2000).
DR EMBL; AF205357; AAG37995.1; -.
DR HSSP; P12111; 2KNT.
DR FlyBase; FBgn0003137; Ppn.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR003598; Ig_c2.
DR InterPro; IPR003600; Ig_Like.
DR InterPro; IPR002223; Kunitz_BPTI.
DR InterPro; IPR000884; TSPI.
DR InterPro; IPR002221; WAP.
DR Pfam; PF00014; Kunitz_BPTI; 3.
DR PRINTS; PR00003; 4DISULPHCORE.
DR PRINTS; PR00759; BASICPTASE.
DR SMART; SM00409; IG; 3.
DR SMART; SM00408; IGC2; 2.
DR SMART; SM00410; IG_Like; 1.
DR SMART; SM00131; KU; 3.
DR SMART; SM00209; TSPI; 7.
DR SMART; SM00217; WAP; 1.
DR PROSITE; PS50279; BPTI_KUNITZ_2; 3.
DR PROSITE; PS50092; TSPI; 3.
KW Matrix protein; Serine protease inhibitor; Signal.
FT SIGNAL 1 26 POTENTIAL.
SQ SEQUENCE 2174 AA; 231936 MW; 038F707952623120 CRC64;
SQ
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DR PRINTS; PR00759; BASICPTASE.

DR SMART; SM00131; KU; 3.

DR PROSITE; PS00280; BPTI_KUNITZ_1; 3.

DR PROSITE; PS0279; BPTI_KUNITZ_2; 3.

KW Serine protease inhibitor.

SQ SEQUENCE 396 AA; 43948 MW; 50F65C8337A003D9 CRC64;

Query Match 25.3%; Score 239.5; DB 6; Length 396;

Best Local Similarity 29.6%; Pred. No. 2.7e-17;

Matches 45; Conservative 24; Mismatches 60; Indels 23; Gaps 1;

QY 5 RSTHDFCLVSKVGRASPRWYNTDGSQCLFYVGGDGNNSNYLTKEECLKKCATV 64

DB 47 RLHSFCALKADGRCPRMIRNFYFIHQCEEFYGGCGNQNRFSLECEECVVR 106

QY 65 TENATGLATSRNAADSSVPSAPRRQDSHSDMFNIEYCTANAVTGPCRASFPRIYF 124

DB 107 YPKA-----KTELEKVLKPDYCHMNEDESLGRCGFVTRY 143

QY 125 DVERNSCNNFIYGGCRGNKNSYSEACMLRC 156

DB 144 NVSSKCEGFYGGCLGNLNNFETLEQCKNTC 175

RESULT 14

Q9DBJ9 PRELIMINARY; PRT; 349 AA.

AC Q9DBJ9; (TREMBlrel. 17, Created)

DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)

DT 01-JUN-2001 (TREMBlrel. 19, Last annotation update)

DE ALPHA 1 MICROGLOBULIN/BIKUNIN.

GN AMBP.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI_TaxID=10090;

RT SEQUENCE FROM N.A.

RC STRAIN=C57BL/6J; TISSUE=LIVER;

RA Kawai J., Shingawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,

RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,

RA Saito T., Okazaki Y., Gojibori T., Bono H., Kasukawa T., Saito R.,

RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,

RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,

RA Schirali L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,

RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,

RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,

RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,

RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,

RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,

RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,

RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,

RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,

RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,

RA Hayashizaki Y.

RT "Functional annotation of a full-length mouse cDNA collection."

RL Nature 409:685-690(2001).

DR EMBL; AK004907; BAB23659.1; -

DR HSSP; P02760; 1BIK.

DR MGD; MGI:88002; Ambp.

DR InterPro; IPR002223; Kunitz_BPTI.

DR InterPro; IPR002345; Lipocalin.

DR InterPro; IPR000566; Lipocalin_cytFABP.

DR Pfam; PF00014; Kunitz_BPTI; 2.

DR Pfam; PF00061; lipocalin; 1.

DR PRINTS; PR00759; BASICPTASE.

DR PRINTS; PR00179; LIPOCALIN.

DR SMART; SM00131; KU; 2.

DR PROSITE; PS0279; BPTI_KUNITZ_2; 2.

DR PROSITE; PS00213; LIPOCALIN; UNKNOWN_1.

KW Serine protease inhibitor.

SQ SEQUENCE 349 AA; 39101 MW; E593222FBC01BC3D CRC64;

Query Match 24.8%; Score 235.5; DB 11; Length 349;

Best Local Similarity 29.7%; Pred. No. 6.2e-17;

Matches 44; Conservative 18; Mismatches 47; Indels 39; Gaps 1;

QY 9 DFCLVSKVGRASPRWYNTDGSQCLFYVGGDGNNSNYLTKEECLKKCATV 68

DB 228 DSCQLNYSSEPCGLGMOERYIYNGASMACETFFYGGCLGNGNFISEKDCLOTCTTAA-- 285

QY 69 TGDLATSRNAADSSVPSAPRRQDSHSDMFNIEYCTANAVTGPCRASFPRIYF 128

DB 286 -----CNLPVQGPCRAFIKLWAFDAQ 308

QY 129 NSCNNFIYGGCRGNKNSYSEACMLRC 156

DB 309 GKCIQHYGGCGNGNKFYSEKECKEYC 336

RESULT 15

Q925W1 PRELIMINARY; PRT; 349 AA.

AC Q925W1; (TREMBlrel. 19, Created)

DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)

DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)

DE ALPHA-1-MICROGLOBULIN/BIKUNIN PRECURSOR.

GN AMBP.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI_TaxID=10090;

RT SEQUENCE FROM N.A.

RC STRAIN=129SV;

RA Lindqvist A., Rouet P., Salier J.P., Akerstrom B.,

RT "The alpha1-microglobulin/bikunin gene: characterization in mouse and

evolution."

RL Gene 234:329-336(1999).

DR EMBL; AF034692; AAD01995.1; -

FT SIGNAL 1 19 POTENTIAL.

FT CHAIN 20 349 ALPHA-1-MICROGLOBULIN/BIKUNIN.

SQ SEQUENCE 349 AA; 39029 MW; CFB9208D37DF0021 CRC64;

Query Match 24.8%; Score 235.5; DB 11; Length 349;

Best Local Similarity 29.7%; Pred. No. 6.2e-17;

Matches 44; Conservative 18; Mismatches 47; Indels 39; Gaps 1;

QY 9 DFCLVSKVGRASPRWYNTDGSQCLFYVGGDGNNSNYLTKEECLKKCATV 68

DB 228 DSCQLNYSSEPCGLGMOERYIYNGASMACETFFYGGCLGNGNFISEKDCLOTCTTAA-- 285

QY 69 TGDLATSRNAADSSVPSAPRRQDSHSDMFNIEYCTANAVTGPCRASFPRIYF 128

DB 286 -----CNLPVQGPCRAFIKLWAFDAQ 308

QY 129 NSCNNFIYGGCRGNKNSYSEACMLRC 156

DB 309 GKCIQHYGGCGNGNKFYSEKECKEYC 336

Search completed: October 18, 2002, 10:35:49

Job time : 33 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: October 18, 2002, 10:33:48 ; Search time 12 Seconds
(without alignments)
548.527 Million cell updates/sec

Title: us-09-218-913d-52

Perfect score: 948

Sequence: 1 ADERSIHDFCLVSKVGRG.....ACMLRCFRQENPPLGSK 170

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues

Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_40.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	948	100.0	252	1	SPT2_HUMAN	O43291 homo sapien
2	663	69.9	252	1	SPT2_MOUSE	Q9W403 mus musculus
3	312	32.9	513	1	SPT1_HUMAN	O43278 homo sapien
4	294	31.0	507	1	SPT1_MOUSE	Q9R097 mus musculus
5	259.5	27.4	306	1	TFPI_MOUSE	O54819 mus musculus
6	249.5	26.3	352	1	AMBP_BOVIN	P00978 bos taurus
7	247.5	26.1	346	1	AMBP_MERUN	O62577 meriones un
8	246.5	26.0	302	1	TFPI_RAT	Q02445 rattus norv
9	244.5	25.8	123	1	IATR_SHEEP	P13371 ovis-aries
10	244.5	25.8	352	1	AMBP_HUMAN	P02760 homo sapien
11	244	25.7	300	1	TFPI_RABIT	P19761 oryctolagus
12	242.5	25.6	337	1	AMBP_PTG	P04366 sus scrofa
13	241.5	25.5	123	1	IATR_HORSE	P04365 equus caball
14	237.5	25.1	349	1	AMBP_RAT	Q64240 rattus norv
15	236.5	24.9	304	1	TFPI_MACMU	Q28864 macaca mula
16	235.5	24.8	349	1	AMBP_MSAU	Q60559 mesocricetu
17	235.5	24.8	349	1	AMBP_MOUSE	Q07456 mus musculus
18	233.5	24.6	304	1	TFPI_HUMAN	P10646 homo sapien
19	214.5	22.6	235	1	TFP2_HUMAN	P48307 homo sapien
20	210	22.2	765	1	APP2_RAT	P15943 rattus norv
21	204.5	21.6	230	1	TFP2_MOUSE	O35536 mus musculus
22	200	21.1	763	1	APP2_HUMAN	Q06481 homo sapien
23	191	20.1	1416	1	YNB1_CAEEL	Q03610 caenorhabdi
24	187.5	19.8	770	1	A4_RAT	P08592 rattus norv
25	186	19.6	751	1	A4_SAISC	Q95241 salminki scl
26	186	19.6	770	1	A4_MOUSE	P05067 homo sapien
27	183.5	19.4	770	1	AMBP_PLEPL	P12023 mus musculus
28	181.5	19.1	355	1	AMBP_PLEPL	P36992 pleuronecte
29	175.5	18.5	69	1	CRPT_BOOMI	P81162 boophilus m
30	174.5	18.4	76	1	A4_MACMU	P29216 macaca mula
31	174.5	18.4	87	1	A4_MACFA	P53601 macaca fasc
32	171.5	18.1	197	1	MCPI_MELCP	P82968 melithaea c
33	170	17.9	58	1	AXP1_ANTAF	P81547 anthoplaura

34	167	17.6	62	1	IP52_ANESU	P10280 anemonia su
35	159	16.8	133	1	EPPI_HUMAN	O95925 homo sapien
36	159	16.8	265	1	TKO1_SHEEP	Q29428 ovis aries
37	156	16.5	64	1	SPT3_HUMAN	P49223 homo sapien
38	156	16.5	164	1	TKO1_BOVIN	Q28201 bos taurus
39	155.5	16.4	133	1	EPPI_MACMU	Q9bd11 macaca mula
40	155	16.4	60	1	IBPS_BOVIN	P00975 bos taurus
41	155	16.4	100	1	BPT2_BOVIN	P04815 bos taurus
42	153	16.1	61	1	IBPI_TACTR	P16044 tachypleus
43	152.5	16.1	100	1	BPT1_BOVIN	P00974 bos taurus
44	152	16.0	65	1	IVB3_VIPAA	P00992 vipera ammo
45	152	16.0	134	1	EPPI_MOUSE	Q9da01 mus musculus

ALIGNMENTS

RESULT 1						
SPT2_HUMAN						
ID	SPT2_HUMAN	STANDARD;	PRT;	252	AA.	
AC	O43291; O00271; O14895; Q969E0;					
DT	16-OCT-2001 (Rel. 40, Created)					
DT	16-OCT-2001 (Rel. 40, Last sequence update)					
DT	01-MAR-2002 (Rel. 41, Last annotation update)					
DE	Kunitz-type protease inhibitor 2 precursor (Hepatocyte growth factor activator inhibitor type 2) (HAI-2) (Placental bikunin).					
DE	SPINT2 OR HAI2 OR KOP.					
GN	Homo sapiens (Human).					
OS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;					
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.					
OX	NCBI_TaxID=9606;					
RN	[1]					
RP	SEQUENCE FROM N.A.					
RX	MEDLINE=98010584; PubMed=9346890;					
RA	Kawaguchi T., Qin L., Shimomura T., Kondo J., Matsumoto K., Denda K.,					
RA	Kitamura N.;					
RT	"Purification and cloning of hepatocyte growth factor activator					
RT	inhibitor type 2, a Kunitz-type serine protease inhibitor.";					
RL	J. Biol. Chem. 272:27558-27564(1997).					
RN	[2]					
RP	SEQUENCE FROM N.A., AND SEQUENCE OF 28-74.					
RC	TISSUE=Placenta;					
RX	MEDLINE=97277372; PubMed=9115294;					
RA	Marlor C.W., Delaria K.A., Davis G., Muller D.K., Greve J.M.,					
RA	Tamburini P.P.;					
RT	"Identification and cloning of human placental bikunin, a novel serine					
RT	protease inhibitor containing two Kunitz domains.";					
RL	J. Biol. Chem. 272:12202-12208(1997).					
RN	[3]					
RP	SEQUENCE FROM N.A.					
RC	TISSUE=Pancratic cancer;					
RX	MEDLINE=98094245; PubMed=9434156;					
RA	Mueller-Pillasch F., Wallrapp C., Bartels K., Varga G., Friess H.,					
RA	Buechler M., Adler G., Gress T.M.;					
RT	"Cloning of a new Kunitz-type protease inhibitor with a putative					
RT	transmembrane domain overexpressed in pancreatic cancer.";					
RL	Biochim. Biophys. Acta 1395:88-95(1998).					
RN	[4]					
RP	SEQUENCE FROM N.A., AND VARIANT LEU-200.					
RC	TISSUE=Colon, and Ovary;					
RA	Straussberg R.;					
RL	Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.					
CC	-!- FUNCTION: INHIBITOR OF HGF ACTIVATOR. ALSO INHIBITS PLASMIN,					
CC	PLASMA AND TISSUE KALLIKREIN, AND FACTOR XIA.					
CC	-!- SUBCELLULAR LOCATION: Type I membrane protein (Potential).					
CC	-!- TISSUE SPECIFICITY: EXPRESSED IN PLACENTA, KIDNEY, PANCREAS,					
CC	PROSTATE, TESTIS, THYMUS, AND TRACHEA.					
CC	-!- DOMAIN: THIS INHIBITOR CONTAINS TWO INHIBITORY DOMAINS.					
CC	-!- SIMILARITY: CONTAINS 2 BPTI/KUNITZ INHIBITOR DOMAINS.					
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EMBL: AB006534; BAA25024.1; -
EMBL: U78095; AAC02781.1; -
EMBL: AF027205; AAB84031.1; -
EMBL: BC001668; AAH01668.1; -
EMBL: BC007705; AAH07705.1; -
EMBL: BC011951; AAH11951.1; -
EMBL: BC011955; AAH11955.1; -
EMBL: BC012868; AAH12868.1; -
HSP: P05067; ITAW.
MIM: 605124; -
InterPro: IPR002223; Kunitz_BPTI.
Pfam: PF00014; Kunitz_BPTI; 2.
PRINTS: PR00759; BASICPTASE.
SMART: SM00131; KU; 2.
PROSITE: PS00280; BPTI_KUNITZ_1; 2.
PROSITE: PS0279; BPTI_KUNITZ_2; 2.
Serine protease inhibitor; Repeat; Glycoprotein; Transmembrane;
Signal; Polymorphism.
FT SIGNAL 1 27
FT CHAIN 28 252 KUNITZ-TYPE PROTEASE INHIBITOR 2.
FT DOMAIN 28 197 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 198 218 POTENTIAL.
FT DOMAIN 219 252 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 38 88 BPTI/KUNITZ INHIBITOR 1.
FT DOMAIN 133 183 BPTI/KUNITZ INHIBITOR 2.
FT DISULFID 38 88 BY SIMILARITY.
FT DISULFID 47 71 BY SIMILARITY.
FT DISULFID 63 84 BY SIMILARITY.
FT ACT_SITE 48 49 REACTIVE BOND (BY SIMILARITY).
FT DISULFID 133 183 BY SIMILARITY.
FT DISULFID 142 166 BY SIMILARITY.
FT DISULFID 158 179 BY SIMILARITY.
FT ACT_SITE 143 144 REACTIVE BOND (BY SIMILARITY).
FT CARBOHYD 57 57 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT VARIANT 94 94 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT VARIANT 200 200 V -> L.
FT CONFLICT 3 3 /FTIQ=VAR_012482.
FT CONFLICT 11 11 Q -> H (IN REF. 3).
FT CONFLICT 53 53 R -> P (IN REF. 1).
FT CONFLICT 240 240 R -> K (IN REF. 3).
FT CONFLICT 240 240 D -> H (IN REF. 3).
SQ SEQUENCE 252 AA; 28228 MW; A7D3360C0EECA2B CRC64;

Query Match 100.0%; Score 948; DB 1; Length 252;
Best Local Similarity 100.0%; Pred. No. 3.1e-83;
Matches 170; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADERSIHDFCLVSKVVGRCRSMRPNWVNTDGSQQLFVYGGCDGNSNNYLTKECLKK 60
DB 28 ADERSIHDFCLVSKVVGRCRSMRPNWVNTDGSQQLFVYGGCDGNSNNYLTKECLKK 87
QY 61 CATVTENATGDLATSNAAADSSVPSAPRQDSHSDMFENYECYCTANAVGPCRASPP 120
DB 88 CATVTENATGDLATSNAAADSSVPSAPRQDSHSDMFENYECYCTANAVGPCRASPP 147
QY 121 RWYFDVERNSNNFYGGCRGNKNSYRSEACMLRCFRQENPPLGSK 170
DB 148 RWYFDVERNSNNFYGGCRGNKNSYRSEACMLRCFRQENPPLGSK 197
RESULT 2
ID SPT2_MOUSE STANDARD; PRT; 252 AA.
AC Q9WU03; Q9WU04; Q9WU05;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Kunitz-type protease inhibitor 2 precursor (Hepatocyte growth factor

DE activator inhibitor type 2) (HAI-2).
GN SPINT2 OR HAI2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.
RC STRAIN=BALB/C;
RX MEDLINE=99160423; PubMed=10049781;
RA Itoh H., Kataoka H., Hamasuna N., Kitamura N., Kono M.;
RT "Hepatocyte growth factor activator inhibitor type 2 lacking the first
RT Kunitz-type serine proteinase inhibitor domain is a predominant
RT product in mouse but not in human";
RL Biochem Biophys Res Commun. 255:740-748(1999).
CC -!- FUNCTION: INHIBITOR OF HGF ACTIVATOR.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein (Potential).
CC -!- ALTERNATIVE PRODUCTS: 3 ISOFORMS; 1 (SHOWN HERE), 2 AND 3; ARE
CC PRODUCED BY ALTERNATIVE SPLICING.
CC -!- TISSUE SPECIFICITY: ISOFORM 2 IS MORE PREDOMINANTLY EXPRESSED THAN
CC ISOFORM 1.
CC -!- DOMAIN: THIS INHIBITOR CONTAINS TWO INHIBITORY DOMAINS.
CC -!- SIMILARITY: CONTAINS 2 BPTI/KUNITZ INHIBITOR DOMAINS.
CC
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EMBL: AF099016; AAD22172.1; -
EMBL: AF099019; AAD22173.1; -
EMBL: AF099020; AAD22174.1; -
HSP: P05067; ITAW.
MGD: MGI:1338031; Spint2.
InterPro: IPR002223; Kunitz_BPTI.
Pfam: PF00014; Kunitz_BPTI; 2.
PRINTS: PR00759; BASICPTASE.
SMART: SM00131; KU; 2.
PROSITE: PS00280; BPTI_KUNITZ_1; 2.
PROSITE: PS0279; BPTI_KUNITZ_2; 2.
Serine protease inhibitor; Repeat; Glycoprotein; Transmembrane;
Signal; Alternative splicing. POTENTIAL.
FT SIGNAL 1 27
FT CHAIN 28 252 KUNITZ-TYPE PROTEASE INHIBITOR 2.
FT DOMAIN 28 197 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 198 218 POTENTIAL.
FT DOMAIN 219 252 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 38 88 BPTI/KUNITZ INHIBITOR 1.
FT DOMAIN 133 183 BPTI/KUNITZ INHIBITOR 2.
FT DISULFID 38 88 BY SIMILARITY.
FT DISULFID 47 71 BY SIMILARITY.
FT DISULFID 63 84 BY SIMILARITY.
FT ACT_SITE 48 49 REACTIVE BOND (BY SIMILARITY).
FT DISULFID 133 183 BY SIMILARITY.
FT DISULFID 142 166 BY SIMILARITY.
FT DISULFID 158 179 BY SIMILARITY.
FT ACT_SITE 143 144 REACTIVE BOND (BY SIMILARITY).
FT CARBOHYD 57 57 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT VARSPLIC 37 93 MISSING (IN ISOFORM 2 AND ISOFORM 3).
FT VARSPLIC 114 128 PKQSNEDLSAIEFN -> CFVELSVAALFLFYA (IN
FT ISOFORM 3).
FT VARSPLIC 129 252 MISSING (IN ISOFORM 3).
SQ SEQUENCE 252 AA; 27914 MW; B2FF4B86924D4F8F CRC64;

Query Match 69.9%; Score 663; DB 1; Length 252;
Best Local Similarity 68.2%; Pred. No. 4.1e-56;
Matches 116; Conservative 21; Mismatches 33; Indels 0; Gaps 0;

QY 1 ADERSIHDFCLVSKVVGRCRSMRPNWVNTDGSQQLFVYGGCDGNSNNYLTKECLKK 60

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Db 28 ASRELDVHSCGSKVGVKCRASIPRWYNTDSCQPEVYGGCEGNNYQSKERCLDK 87
QY 61 CATVTENATGCDLSDNAADSVSPASPRDSDSHSDMFENYEEYCTANAVTGPCRASFP 120
Db 88 CAGVTENTDDWARRNGADSSVLSVPRQKSEDLSAEIFNFEYECVPRAVTGPCRAAPP 147
QY 121 RWFYDVERNSCNFIYGGCGKNGKNSYSEACMLRCFROQENPPLPLGSK 170
Db 148 RWDYDEKNSCISFIYGGCGKNGKNSYLSQACMQHSCGKQMHPLTPGLK 197

RESULT 3
SPTL_HUMAN
ID SPTL_HUMAN STANDARD; PRT; 513 AA.
AC O43278;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE Kunitz-type protease inhibitor 1 precursor (Hepatocyte growth factor
DE activator inhibitor type 1) (HAI-1).
GN SPINT1 OR HAI1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97197808; PubMed=9045658;
RA Shimomura T., Denda K., Kitamura A., Kawaguchi T., Kito M., Kondo J.,
RA Kagaya S., Qin L., Takata H., Miyazawa K., Kitamura N.;
RT "Hepatocyte growth factor activator inhibitor, a novel Kunitz-type
RT serine protease inhibitor.";
RL J. Biol. Chem. 272:6370-6376(1997).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Colon;
RA Strausberg R.;
RL Submitted (Mar.-2001) to the EMBL/GenBank/DBJ databases.
RN [3]
RP PARTIAL SEQUENCE, AND CHARACTERIZATION.
RC TISSUE=Milk;
RX MEDLINE=99303582; PubMed=10373425;
RA Lin C.Y., Anders J., Johnson M., Dickson R.B.;
RT "Purification and characterization of a complex containing matrilptase
RT and a Kunitz-type serine protease inhibitor from human milk.";
RL J. Biol. Chem. 274:19237-19242(1999).
CC -!- FUNCTION: INHIBITOR OF HGF ACTIVATOR. ALSO ACTS AS AN INHIBITOR OF
CC MATRIPTASE (ST14).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- DOMAIN: THIS INHIBITOR CONTAINS TWO INHIBITORY DOMAINS.
CC -!- SIMILARITY: CONTAINS 1 LDL-RECEPTOR CLASS A DOMAIN.
CC -!- SIMILARITY: CONTAINS 2 BPTI/KUNITZ INHIBITOR DOMAINS.
CC
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CC
CC EMBL; AB000095; BAA25014.1;
CC EMBL; BC004140; AA04140.1;
CC HSP; P31713; 1SPH.
CC MIM; 605123;
CC InterPro; IPR002223; Kunitz_BPTI.
CC InterPro; IPR002172; LDL_recept_A.
CC Pfam; PF00014; Kunitz_BPTI; 2.
CC Pfam; PF00057; ldl_recept_a; 1.
CC PRINTS; PR00759; BASICPTASE.
CC SMART; SM00131; KU; 2.
CC SMART; SM00192; LDLa; 1.

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DR PROSITE; PS00280; BPTI_KUNITZ_1; 2.
DR PROSITE; PS02079; BPTI_KUNITZ_2; 2.
DR PROSITE; PS01209; LDLRA_1; 1.
DR PROSITE; PS00068; LDLRA_2; 1.
KW Serine protease inhibitor; Repeat; Glycoprotein; Signal.
FT SIGNAL 1 35
FT CHAIN 36 513 KUNITZ-TYPE PROTEASE INHIBITOR 1.
FT DOMAIN 250 300 BPTI/KUNITZ INHIBITOR 1.
FT DOMAIN 318 354 LDL-RECEPTOR CLASS A.
FT DOMAIN 375 425 BPTI/KUNITZ INHIBITOR 2.
FT DISULFID 250 300 BY SIMILARITY.
FT DISULFID 259 283 BY SIMILARITY.
FT DISULFID 275 296 BY SIMILARITY.
FT ACT_SITE 260 261 REACTIVE BOND (BY SIMILARITY).
FT DISULFID 375 425 BY SIMILARITY.
FT DISULFID 384 408 BY SIMILARITY.
FT ACT_SITE 385 386 REACTIVE BOND (BY SIMILARITY).
FT CARBOHYD 56 66 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 235 235 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 507 507 N-LINKED (GLCNAC. .) (POTENTIAL).
SQ SEQUENCE 513 AA; 56885 MW; D6E05F3A5885CDDD CRC64;

Query Match 32.9%; Score 312; DB 1; Length 513;
Best Local Similarity 33.5%; Pred. No. 2.3e-22;
Matches 67; Conservative 24; Mismatches 71; Indels 38; Gaps 5.

QY 5 RSHDFCLVSKVVGCRASMPRWYNTDSCQPEVYGGCEGNNYLTKEECLKKCATV 64
Db 244 KOTEDYCLASNKVYGRGSGFSFPRWYDPTQICKYVGGCLGNKNNYREEICILACRGV 303
QY 65 -----TENATGDLATSRNAADS-----SVPSAPRRQDS---EDHSSDMFNY 102
Db 304 QGPMERHPVCSGTCQPTQFCRSCNGCCIDSFLECDTTPNCPDASDEACEKYTSFDEL 363
QY 103 EE-----YCTANAVTGPCRASFPWYFDVVERNSCNFIYGGCGKNGKNSYSEACML 154
Db 364 QRHFPSDKGHCVLDPTDGLCKESIPRWYNPFSEHCAFTYGGCYGKNNFEEQOOLE 423
QY 155 RC-----FRQENPPLP 166
Db 424 SCRGISKDVFGRLRREIP 443

RESULT 4
SPTL_MOUSE
ID SPTL_MOUSE STANDARD; PRT; 507 AA.
AC Q9R097;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Kunitz-type protease inhibitor 1 precursor (Hepatocyte growth factor
DE activator inhibitor type 1) (HAI-1).
GN SPINT1 OR HAI1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/C;
RA Itoh H., Kataoka H., Koono H.;
RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: INHIBITOR OF HGF ACTIVATOR (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: Secreted (By similarity).
CC -!- DOMAIN: THIS INHIBITOR CONTAINS TWO INHIBITORY DOMAINS.
CC -!- SIMILARITY: CONTAINS 1 LDL-RECEPTOR CLASS A DOMAIN.
CC -!- SIMILARITY: CONTAINS 2 BPTI/KUNITZ INHIBITOR DOMAINS.
CC
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ERX	MEDLINE=84133808; PubMed=6199276;	22	CARBOHYD	223	N-LINKED (GLCNAc. . .) (POTENTIAL).
RA	Hochstrasser K., Albrecht G.J., Schoenberger O.L., Wachter E.;	23	CARBOHYD	250	N-LINKED (GLCNAc. . .).

Db 182 QKGDYVNTQITVTDRTVNNVVIPQTAKPSQWDYDGPSS-----WCLEPADSLCKA 233

Qy 118 SFRWFDFVERNSCNFIYGCGRCGNKNYSRSEACMLRC 156
I I L I : : I I I I I I : : : I I

Dd 234 SEKREYNPAIGKCRQFNFTGCGGNNNFTTKDCNRAC 272

RESULT 9

ID	IATR_SHEEP	STANDARD;	PRT;	123 AA.
AC	PI337L:			
DT	01-JAN-1990 (Rel. 13, Created)			
DT	01-JAN-1990 (Rel. 13, Last sequence update)			
DT	16-OCT-2001 (Rel. 40, Last annotation update)			
DE	Inter-alpha-trypsin inhibitor (ITI) (GIK-14) (Inhibitory fragment of ITI) (Fragment).			
DE	Ovis aries (Sheep), and			
OS	Capra hircus (Goat).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;			
OX	Bovidae; Caprinae; Ovis.			
OX	NCBI_TaxID=9940, 9925;			
RN	[1]			
RP	SEQUENCE.			
RC	SPECIES=Sheep;			
RC	MEDLINE=87299012; PubMed=2441725;			
RX	Rasp G., Hochstrasser K., Wachter E., Reisinger P.W.M.;			
RT	"The amino-acid sequence of the trypsin-released inhibitor from sheep inter-alpha-trypsin inhibitor";			
RT	Biol. Chem. Hoppe-Seyler 368:727-731(1987). [2]			
RN	SEQUENCE.			
RC	SPECIES=C.hircus;			
RC	MEDLINE=90105540; PubMed=2481505;			
RX	Rasp G., Hochstrasser K., Gerl C., Wachter E.;			
RA	"Primary structure of a proteinase inhibitor released from goat serum inter-alpha-trypsin inhibitor.";			
RT	Biochim. Biophys. Acta 999:335-337(1989).			
CC	-1- FUNCTION: THIS INHIBITORY FRAGMENT, RELEASED FROM NATIVE ITI AFTER LIMITED PROTEOLYSIS WITH TRYPSIN, CONTAINS TWO HOMOLOGOUS DOMAINS WHEREAS THE SECOND DOMAIN IS A STRONG INHIBITOR OF TRYPSIN, THE FIRST DOMAIN INTERACTS WEAKLY WITH PMN-GRANULOCYTIC ELASTASE AND NOT AT ALL WITH PANCREATIC ELASTASE.			
CC	-1- MISCELLANEOUS: THE AMINO ACID AT POSITION P2' (17) APPEARS TO DETERMINE THE SPECIFICITY OF THE INHIBITION OF DOMAIN 1.			
CC	INHIBITORS WITH METHIONINE IN THIS POSITION INTERACT WEAKLY WITH CHYMOTRYPSIN AND ELASTASE; THOSE WITH LEUCINE INTERACT STRONGLY.			
CC	-1- SIMILARITY: CONTAINS 2 BPTI/KUNITZ INHIBITOR DOMAINS.			
DR	PIR; A29652; A29652.			
DR	HSP; P02760; 1B1K.			
DR	InterPro; IPR002223; Kunitz_BPTI.			
DR	Pfam; PF000014; Kunitz_BPTI; 2.			
DR	SMART; SM00131; KU; 2.			
DR	PROSITE; PS00280; BPTI_KUNITZ_1; 2.			
DR	PROSITE; PS50279; BPTI_KUNITZ_2; 2.			
KW	Plasma; Glycoprotein; Serine protease inhibitor; Repeat.			
FT	NON_TER 1			
FT	DOMAIN 5			
FT	DOMAIN 61			
FT	DISULFID 5			
FT	DISULFID 14			
FT	DISULFID 30			
FT	DISULFID 61			
FT	DISULFID 70			
FT	DISULFID 86			
FT	ACT_SITE 15			
FT	ACT_SITE 71			
FT	CARBHYD 24			
FT	NON_TER 123			
SEQ	SEQUENCE 123 AA; 13686 MW; 295038173F22D2D1 CRC64;			

Query Match 25.8%; Score 244.5; DB 1; Length 123;

RT blood protein pre-alpha-inhibitor.";
RL J. Biol. Chem. 266:747-751(1991).
RN [16]
RX X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS) OF 230-339.
RA MEDLINE=98227321; PubMed=9566199;
RA Xu Y., Carr P.D., Guss J.M., Ollis D.L.;
RT "the crystal structure of bikunin from the inter-alpha-inhibitor
complex: a serine protease inhibitor with two Kunitz domains.";
RL J. Mol. Biol. 276:955-966(1998).
CC !- FUNCTION: ALPHA-1-MICROGLOBULIN OCCURS IN MANY PHYSIOLOGICAL
CC FLUIDS INCLUDING PLASMA, URINE, AND CEREBROSPINAL FLUID. IT
CC APPEARS NOT ONLY AS A FREE MONOMER BUT ALSO IN COMPLEXES WITH IGA
CC AND ALBUMIN.
CC !- FUNCTION: INTER-ALPHA-TRYPsin INHIBITOR, PRESENT IN PLASMA AND
CC URINE, INHIBITS TRYPSIN, PLASMIN, AND LYSOSOMAL GRANULOCYTIC
CC ELASTASE. ADDITIONAL PROTEOLYTIC PROCESSING IN THE KIDNEY AND/OR
CC URINE CAN PRODUCE FURTHER AMINO- AND CARBOXYL-END MODIFICATIONS
CC IN ITS SEQUENCE.
CC !- SUBUNIT: I-ALPHA-I plasma protease inhibitors are assembled from
CC one or two heavy chains (H1, H2 or H3) and one light chain,
CC bikunin. Inter-alpha-inhibitor (I-ALPHA-I) is composed of H1, H2
CC and bikunin, inter-alpha-like inhibitor (I-ALPHA-LI) of H2 and
CC bikunin, and pre-alpha-inhibitor (P-ALPHA-I) of H3 and bikunin (by
CC similarity).
CC !- PTM: THE PRECURSOR IS PROTEOLYTICALLY PROCESSED INTO TWO
CC SEPARATELY FUNCTIONING PROTEINS.
CC !- PTM: Alpha-1-microglobulin contains a covalently linked brown-
CC yellow chromophore.
CC !- PTM: ADDITION OF GLYCOSAMINOGLYCAN CHONDROITIN SULFATE, ALLOWS
CC CROSS-LINKING BETWEEN THE DIFFERENT COMPONENTS.
CC !- MISCELLANEOUS: IN VITRO, THE FIRST TWELVE RESIDUES OF THE AMINO
CC END OF THE INHIBITOR APPEAR TO HAVE A REACTIVE SITE CAPABLE OF
CC INHIBITING THE ACTIVITY OF A NUMBER OF ENZYMES. ITS IN VIVO
CC FUNCTION IS NOT KNOWN.
CC !- SIMILARITY: IN THE N-TERMINAL SECTION; BELONGS TO THE LIPOCALIN
CC FAMILY
CC !- SIMILARITY: CONTAINS 2 BPTI/KUNITZ INHIBITOR DOMAINS.
CC
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; X54816; CAA38585.1; -
CC EMBL; X54817; CAA38585.1; JOINED.
CC EMBL; X54818; CAA38585.1; JOINED.
CC EMBL; X04225; CAA27803.1; -
CC EMBL; M88249; AAA59196.1; -
CC EMBL; M88165; AAA59196.1; JOINED.
CC EMBL; M88243; AAA59196.1; JOINED.
CC EMBL; M88244; AAA59196.1; JOINED.
CC EMBL; M88246; AAA59196.1; JOINED.
CC EMBL; M88247; AAA59196.1; JOINED.
CC EMBL; X04494; CAA28182.1; -
CC EMBL; X54817; CAA38586.1; -
CC PIR; A03217; HCHU
CC PIR; A25303; A25303.
CC PIR; S13433; S13433.
CC PIR; S10717; S10717.
CC PDB; 1BIK; 16-MAR-99.
CC GlycositedB; P02760; -
CC SWISS-2DPAGE; P02760; HUMAN.
CC Siena-2DPAGE; P02760; -
CC MIM; 176870; -
CC InterPro; IPR002223; Kunitz_BPTI.
CC InterPro; IPR002345; Lipocalin.
CC InterPro; IPR000566; Lipocalin_cytFABP.
CC Pfam; PF00014; Kunitz_BPTI; 2.
CC Pfam; PF00061; Lipocalin; 1.

Query Match 25.8%; Score 244.5; DB 1; Length 352;
Best Local Similarity 32.4%; Pred. No. 4e-16;
Matches 48; Conservative 14; Mismatches 47; Indels 39; Gaps 1;

QY 9 DCLVSKVVGRCRASPRWVNTDSCQLFVYGGCDGHSNNYLYKECLKCAVTYENA 68
DB 229 DSCQLGYSAGPCMGMTSRFYNGTSMACETFOYGGCMGNFNFTKECLQTCRTVAA-- 286
QY 69 TGDLATSRNAADSSVPSAPRRQDSHSDMFENYEBYCTANAVTGPCRASFPFWYFDVER 128
DB 287 -----CNLPVIRGCPRAFIQLWAEDAVK 309

QY 129 NSCNNFIYGGCRGNKNSYRSEACMLRC 156
DB 310 GKCVLPYGGCGCGNGNKFYSEKREYVC 337

RESULT 11
TFPI_RABIT STANDARD; PRT; 300 AA.
AC PL9761; Q28828;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Tissue factor pathway inhibitor precursor (TFPI) (lipoprotein-
DE associated coagulation inhibitor) (LACI) (Extrinsic pathway inhibitor)
DE (EPI).
GN TFPI.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=91057146; PubMed=2136251;
RA Wesselschmidt R.L., Girard T.J., Broze G.J. Jr.;
RT "cDNA sequence of rabbit lipoprotein-associated coagulation
RT inhibitor".
RL Nucleic Acids Res. 18:6440-6440(1990).
RN [2]
RP REVISIONS TO 72; 211 AND 218.
RC TISSUE=Liver;
RX MEDLINE=92335027; PubMed=1630940;
RA Warn-Cramer B.J., Broze G.J. Jr., Komives E.A.;
RT "cDNA sequence of rabbit tissue factor pathway inhibitor";
RL Nucleic Acids Res. 20:3548-3548(1992).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RX MEDLINE=93276427; PubMed=8503123;
RA Belaaouaj A., Kuppawamy M.N., Birktoft J.J., Bajaj S.P.;
RT "Revised cDNA sequence of rabbit tissue factor pathway inhibitor";
RL Thromb. Res. 69:547-553(1993).
CC !- FUNCTION: INHIBITS FACTOR X (X(A)) DIRECTLY AND, IN A XA-DEPENDENT
CC WAY, INHIBITS VII(A)/TISSUE FACTOR ACTIVITY, PRESUMABLY BY FORMING
CC A QUATERNARY X(A)/LACI/VII(A)/TF COMPLEX. IT POSSESSES AN
CC ANTITHROMBOTIC ACTION AND ALSO THE ABILITY TO ASSOCIATE WITH
CC LIPOPROTEINS IN PLASMA.
CC !- SUBCELLULAR LOCATION: Secreted.
CC !- DOMAIN: THIS INHIBITOR CONTAINS THREE INHIBITORY DOMAINS.
CC !- SIMILARITY: CONTAINS 3 BPTI/KUNITZ INHIBITOR DOMAINS.
CC
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CC use by non-profit institutions as long as its content is in no way
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CC
CC EMBL; X54708; CAA38515.1; ALT_SEQ.
CC EMBL; S61902; AAB26836.1; -
CC
CC DR EMBL; X54708; CAA38515.1; ALT_SEQ.
CC DR EMBL; S61902; AAB26836.1; -

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DR PIR; S12143; S12143.
DR HSP; P10646; 1TFX.
DR InterPro: IPR002223; Kunitz_BPTI.
DR Pfam; PF00014; Kunitz_BPTI; 3.
DR PRINTS; PR00759; BASICPTASE.
DR SMART; SM00131; KU; 3.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 3.
DR PROSITE; PS00279; BPTI_KUNITZ_2; 3.
KW Serine protease inhibitor; Glycoprotein; Repeat; Blood coagulation;
KW Signal.
FT SIGNAL 1 24
FT CHAIN 25 300
FT DOMAIN 50 100
FT DOMAIN 121 171
FT DOMAIN 213 263
FT TISSUE FACTOR PATHWAY INHIBITOR.
FT BPTI/KUNITZ INHIBITOR 1
FT (VII(A)/TISSUE FACTOR BINDING SITE).
FT BPTI/KUNITZ INHIBITOR 2
FT (FACTOR X(A) BINDING SITE).
FT BPTI/KUNITZ INHIBITOR 3
FT (BY SIMILARITY).
FT BY SIMILARITY.
FT BY SIMILARITY.
FT BY SIMILARITY.
FT BY SIMILARITY.
FT REACTIVE BOND (BY SIMILARITY).
FT BY SIMILARITY.
FT BY SIMILARITY.
FT BY SIMILARITY.
FT REACTIVE BOND (BY SIMILARITY).
FT BY SIMILARITY.
FT BY SIMILARITY.
FT BY SIMILARITY.
FT REACTIVE BOND (BY SIMILARITY).
FT N-LINKED (GLCNAC. .) (POTENTIAL).
FT N-LINKED (GLCNAC. .) (POTENTIAL).
FT N-LINKED (GLCNAC. .) (POTENTIAL).
FT MISSING (IN REF. 3).
FT PSI -> RNLS (IN REF. 3).
FT CONFLICT 269 272
FT SEQUENCE 300 AA; 34435 MW; A08DE36537708CA6 CRC64;
SQ
Query Match 25.7%; Score 244; DB 1; Length 300;
Best Local Similarity 30.0%; Pred. No. 3.7e-16;
Matches 48; Conservative 23; Mismatches 61; Indels 28; Gaps 2;
QY 4 ERSIHDFCLVSKVVGRCASMPRWVNVTDGSCQLFVYGGDGNSSNNYLTKEELKKCAT 63
Db 43 QKPTSFCAKVDGDCRAYIKRFFENILTHQCEFIYGGCEGNRNFESLECKEKAR 102
QY 64 VTENATGDLATSNRADSVSPAPROQSDSHSDMFNEEYCTANAVTGPCRASEPRRY 123
Db 103 DYPKMTTKLTFQKGKPD-----FCFLEEDPGICRGYITRYF 138
QY 124 FQVERNSCNFIYGGCGKGNKNSYRSEACMLRCFRQQENP 163
Db 139 YNNQSKQCFERFYGGCLGNLNFESLECKNTC-----ENP 174
RESULT 12
AMBP.PIG
ID AMBP.PIG STANDARD; PRT; 337 AA.
AC P04366; P34954;
DT 20-MAR-1987 (Rel. 04, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE AMBP protein precursor [Contains: Alpha-1-microglobulin; Inter-alpha-
DE trypsin inhibitor light chain (ITI-LC) (Bikunin) (HI-30) (EI-14)]
DE (Fragment).
GN AMBP OR ITIL.
OS Sus scrofa (Pig).
OC Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
[1]
RN SEQUENCE FROM N.A.
RX MEDLINE=90353595; PubMed=1696914;
RA Gebhard W., Schreitmuller T., Vetr H., Wachter E., Hochstrasser K.;

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RT "Complementary DNA and deduced amino acid sequences of porcine alpha
RT 1-microglobulin and bikunin.";
RL FEBS Lett. 269:32-36(1990).
RN [2]
RC SEQUENCE OF 2-337 FROM N.A.
PC TISSUE=Liver;
RX MEDLINE=91113729; PubMed=1703444;
RA Tavakkol A.;
RT "Molecular cloning of porcine alpha 1-microglobulin/HI-30 reveals
RT developmental and tissue-specific expression of two variant messenger
RT ribonucleic acids.";
RL Biochim. Biophys. Acta 1088:47-56(1991).
RN [3]
RP SEQUENCE OF 212-334.
RX MEDLINE=85225967; PubMed=2408637;
RA Hochstrasser K., Wachter E., Albrecht G.J., Reisinger P.;
RT "Kunitz-type proteinase inhibitors derived by limited proteolysis of
RT the inter-alpha-trypsin inhibitor, X. The amino-acid sequences of the
RT trypsin-released inhibitors from horse and pig inter-alpha-trypsin
RT inhibitors.";
RL Biol. Chem. Hoppe-Seyler 366:473-478(1985).
CC -!- FUNCTION: ALPHA-1-MICROGLOBULIN OCCURS IN MANY PHYSIOLOGICAL
CC FLUIDS INCLUDING PLASMA, URINE, AND CEREBROSPINAL FLUID. IT
CC APPEARS NOT ONLY AS A FREE MONOMER BUT ALSO IN COMPLEXES WITH IGA
CC AND ALBUMIN.
CC -!- FUNCTION: INTER-ALPHA-TRYPsin INHIBITOR, PRESENT IN PLASMA AND
CC URINE. INHIBITS TRYPSIN, PLASMIN, AND LYSOSOMAL GRANULOCYTIC
CC ELASTASE.
CC -!- SUBUNIT: I-ALPHA-I plasma protease inhibitors are assembled from
CC one or two heavy chains (H1, H2 or H3) and one light chain,
CC bikunin. Inter-alpha-inhibitor (I-ALPHA-I) is composed of H1, H2
CC and bikunin, inter-alpha-like inhibitor (I-ALPHA-LI) of H2 and
CC bikunin, and pre-alpha-inhibitor (P-ALPHA-I) of H3 and bikunin (By
CC similarity).
CC -!- PTM: THE PRECURSOR IS PROTEOLYTICALLY PROCESSED INTO TWO
CC SEPARATELY FUNCTIONING PROTEINS.
CC -!- PTM: Alpha-1-microglobulin contains a covalently linked brown-
CC yellow chromophore.
CC -!- SIMILARITY: IN THE N-TERMINAL SECTION; BELONGS TO THE LIPOCALIN
CC FAMILY.
CC -!- SIMILARITY: CONTAINS 2 BPTI/KUNITZ INHIBITOR DOMAINS.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; X53685; CAA37725.1; -.
DR EMBL; X52087; CAA36306.1; -.
DR PIR; A01208; TIPGB1.
DR PIR; S11066; S11066.
DR HSP; P02760; IBIK.
DR InterPro: IPR002223; Kunitz_BPTI.
DR InterPro: IPR000566; Lipocln_cytfabp.
DR Pfam; PF00014; Kunitz_BPTI; 2.
DR Pfam; PF00061; lipocalin; 1.
DR SMART; SM00131; KU; 2.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 2.
DR PROSITE; PS00279; BPTI_KUNITZ_2; 2.
DR PROSITE; PS00213; LIPOCALIN; 1.
KW Glycoprotein; Plasma; Signal; Serine protease inhibitor; Repeat;
KW Lipocalin.
FT NON_TER 1 1
FT SIGNAL <1 4
FT CHAIN 5 188
FT CHAIN 191 337
FT DOMAIN 216 266
FT DOMAIN 272 322
FT BINDING 38 38
BY SIMILARITY.
ALPHA-1-MICROGLOBULIN.
INTER-ALPHA-TRYPSIN INHIBITOR LIGHT
CHAIN.
BPTI/KUNITZ INHIBITOR 1.
BPTI/KUNITZ INHIBITOR 2.
CHROMOPHORE (BY SIMILARITY).

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FT DISULFID 76 173 BY SIMILARITY.
FT DISULFID 216 266
FT DISULFID 225 249
FT DISULFID 241 262
FT DISULFID 272 322
FT DISULFID 281 305
FT DISULFID 297 318
FT DISULFID 100 100
FT CARBOHYD 235 235
FT ACT_SITE 226 227
FT ACT_SITE 282 283
FT CONFLICT 49 49
FT CONFLICT 259 259
FT CONFLICT 270 270
FT CONFLICT 278 278
FT CONFLICT 283 283
FT CONFLICT 285 286
FT CONFLICT 293 293
FT CONFLICT 311 311
FT CONFLICT 315 315
SQ SEQUENCE 337 AA; 37690 MW; 1F630FF98E3CD70F CRC64;

N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .).
INHIBITORY SITE (PI) (CHYMOTRYPSIN, ELASTASE).
T -> M (IN REF. 2).
E -> Q (IN REF. 3).
E -> S (IN REF. 3).
S -> Q (IN REF. 3).
G -> A (IN REF. 3).
FQ -> IR (IN REF. 3).
V -> A (IN REF. 3).
Q -> K (IN REF. 3).
E -> Q (IN REF. 3).

Query Match 25.6%; Score 242.5; DB 1; Length 337;
Best Local Similarity 31.8%; Pred. No. 5.9e-16;
Matches 47; Conservative 19; Mismatches 43; Indels 39; Gaps 1;

QY 9 DFCLVSKVVGRCRASPRWYVNTDSCOLFVYGGDGNMNYLTKEECLKKCATVTENA 68
DB 214 DSCQLGYSGPCLGIMTKIRFYNGSSMACETFFHYGGMGNGNMFVSEKECLQTCRTV---- 269
QY 69 TGDLATSRNAADSSVPSAPRRQDSEHSDMFENYEYCTANAVTGPCRASFFRWYFDVER 128
DB 270 -----EACSLPIVSGPCRGFFQLWAFDAVQ 294

QY 129 NSCNNFIYGGCRGNKNSYRSEACMLRC 156
DB 295 GKCVLFYGGCGNGNQFYSEKECKYC 322

RESULT 13
IATR_HORSE
ID IATR_HORSE STANDARD; PRT; 123 AA.
AC P04365;
DT 20-MAR-1987 (Rel. 04, Created)
DT 20-MAR-1987 (Rel. 04, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Inter-alpha-trypsin inhibitor (ITI) (HI-14) (Inhibitory fragment of DE .ITI) (fragment).
OS Equus caballus (Horse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
OX NCBI_TaxID=9796;
RN [1]
RP SEQUENCE.
RX MEDLINE=85225967; PubMed=2408637;
RA Hochstrasser K., Wächter E., Albrecht G.J., Reisinger P.;
RT "Kunitz-type proteinase inhibitors derived by limited proteolysis of the inter-alpha-trypsin inhibitor, X. The amino-acid sequences of the trypsin-released inhibitors from horse and pig inter-alpha-trypsin inhibitors.";
RL Biol. Chem. Hoppe-Seyler 366:473-478 (1985).
CC -!- FUNCTION: THIS INHIBITORY FRAGMENT, RELEASED FROM NATIVE ITI AFTER LIMITED PROTEOLYSIS WITH TRYPSIN, CONTAINS TWO HOMOLOGOUS DOMAINS. WHEREAS THE SECOND DOMAIN IS A STRONG INHIBITOR OF TRYPSIN, THE FIRST DOMAIN INTERACTS WEAKLY WITH PMN-GRANULOCYTIC ELASTASE AND NOT AT ALL WITH PANCREATIC ELASTASE.
CC -!- MISCELLANEOUS: THE AMINO ACID AT POSITION P2' (17) APPEARS TO DETERMINE THE SPECIFICITY OF THE INHIBITION OF DOMAIN I.
CC INHIBITORS WITH METHIONINE IN THIS POSITION INTERACT WEAKLY WITH CHYMOTRYPSIN AND ELASTASE; THOSE WITH LEUCINE INTERACT STRONGLY.
CC -!- SIMILARITY: CONTAINS 2 BPTI/KUNITZ INHIBITOR DOMAINS.
DR PIR; A01210; TIH01.

DR HSP; P02760; IBIK.
DR InterPro; IPR002223; Kunitz_BPTI.
DR Pfam; PF00014; Kunitz_BPTI; 2.
DR SMART; SM00131; KU; 2.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 2.
DR PROSITE; PS00279; BPTI_KUNITZ_2; 2.
KW Plasma; Glycoprotein; Serine protease inhibitor; Repeat.
FT NON_TER 1 1
FT DOMAIN 5 55 BPTI/KUNITZ INHIBITOR 1.
FT DOMAIN 61 111 BPTI/KUNITZ INHIBITOR 2.
FT DISULFID 5 55
FT DISULFID 14 38
FT DISULFID 30 51
FT DISULFID 61 111
FT DISULFID 70 94
FT DISULFID 86 107
FT ACT_SITE 15 16 INHIBITORY SITE (PI) (CHYMOTRYPSIN, ELASTASE).
FT ACT_SITE 71 72 INHIBITORY SITE (PI) (TRYPSIN).
FT CARBOHYD 24 24 N-LINKED (GLCNAC. . .).
FT NON_TER 123 123
SQ SEQUENCE 123 AA; 13510 MW; CEIA9120774411D5 CRC64;

Query Match 25.5%; Score 241.5; DB 1; Length 123;
Best Local Similarity 31.8%; Pred. No. 2.4e-16;
Matches 47; Conservative 15; Mismatches 47; Indels 39; Gaps 1;

QY 9 DFCLVSKVVGRCRASPRWYVNTDSCOLFVYGGDGNMNYLTKEECLKKCATVTENA 68
DB 3 DSCQLDHAQGCPLGIMTSRYFYNGTSMACETFFYGGCLGNGNMFASQKECLQTCRTVAA-- 60
QY 69 TGDLATSRNAADSSVPSAPRRQDSEHSDMFENYEYCTANAVTGPCRASFFRWYFDVER 128
DB 61 -----CNLPIVQGPCRAFIRLWAFDAQAQ 83

QY 129 NSCNNFIYGGCRGNKNSYRSEACMLRC 156
DB 84 GKCVLFYGGCGNGNKFSQKECKYC 111

RESULT 14
AMBP_RAT
ID AMBP_RAT STANDARD; PRT; 349 AA.
AC Q64240; Q63336; P19603;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE AMBP protein precursor [Contains: Alpha-1-microglobulin; Inter-alpha-trypsin inhibitor light chain (ITI-LC) (Bikunin) (HI-30); Trypsin].
GN AMBP OR ITIL.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX TISSUE=Liver;
RX MEDLINE=92182014; PubMed=1371936;
RA Lindqvist A., Bratt T., Altieri M., Kastern W., Akerstrom B.;
RT "Rat alpha 1-microglobulin: co-expression in liver with the light chain of inter-alpha-trypsin inhibitor.";
RL Biochim. Biophys. Acta 1130:63-67 (1992).
RN [2]
RP SEQUENCE OF 141-195 FROM N.A.
RX MEDLINE=87033744; PubMed=2429963;
RA Kastern W., Bjoerck L., Akerstrom B.;
RT "Developmental and tissue-specific expression of alpha 1-microglobulin mRNA in the rat.";
RL J. Biol. Chem. 261:15070-15074 (1986).
RN [3]
RP SEQUENCE OF 283-343, AND CHARACTERIZATION.
RX MEDLINE=89053978; PubMed=3263966;

RA Kido H., Yokogoshi Y., Katunuma N.;
 RT "Kunitz-type protease inhibitor found in rat mast cells. Purification,
 properties, and amino acid sequence.";
 RL J. Biol. Chem. 263:18104-18107(1988).
 RN [4]
 RP PROCESSING.
 RX MEDLINE=94148892; PubMed=7508921;
 RA Itoh H., Ide H., Ishikawa N., Nawa Y.;
 RT "Mast cell protease inhibitor, trypstatin, is a fragment of
 inter-alpha-trypsin inhibitor light chain.";
 RL J. Biol. Chem. 269:3818-3822(1994).
 CC -!- FUNCTION: ALPHA-1-MICROGLOBULIN OCCURS IN MANY PHYSIOLOGICAL
 CC FLUIDS INCLUDING PLASMA, URINE, AND CEREBROSPINAL FLUID. IT
 CC APPEARS NOT ONLY AS A FREE MONOMER BUT ALSO IN COMPLEXES WITH IGA
 CC AND ALBUMIN (BY SIMILARITY).
 CC -!- FUNCTION: INTER-ALPHA-TRYPsin INHIBITOR, PRESENT IN PLASMA AND
 CC URINE, INHIBITS TRYPSIN, PLASMIN, AND LYSOSOMAL GRANULOCYTIC
 CC ELASTASE (BY SIMILARITY).
 CC -!- FUNCTION: Trypsstatin is a trypsin inhibitor. It inhibits blood
 CC coagulation factor Xa and trypsinase about 100-fold more rapidly
 CC than porcine pancreatic trypsin and chymase. It is a monomer but
 CC is also found in mast cells as a complex with tryptase.
 CC -!- SUBUNIT: I-ALPHA-1 plasma protease inhibitors are assembled from
 CC one or two heavy chains (H1, H2 or H3) and one light chain,
 CC bikunin. Inter-alpha-inhibitor (I-ALPHA-I) is composed of H1, H2
 CC and bikunin, inter-alpha-like inhibitor (I-ALPHA-LI) of H2 and
 CC bikunin, and pre-alpha-inhibitor (P-ALPHA-I) of H3 and bikunin (By
 CC similarity).
 CC -!- SUBCELLULAR LOCATION: Trypsstatin is present in mast cell granules.
 CC -!- PTM: The precursor is proteolytically processed into separately
 CC functioning proteins.
 CC -!- PTM: Alpha-1-microglobulin contains a covalently linked brown-
 CC Yellow chromophore (By similarity).
 CC -!- PTM: Heavy chains are interlinked with bikunin via a chondroitin
 CC 4-sulfate bridge to the their C-terminal aspartate (By
 CC similarity).
 CC -!- SIMILARITY: IN THE N-TERMINAL SECTION; BELONGS TO THE LIPOCALIN
 CC FAMILY.
 CC -!- SIMILARITY: CONTAINS 2 BPTI/KUNITZ INHIBITOR DOMAINS.
 CC
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 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC
 CC EMBL; S87544; AAB21782.1; -;
 CC EMBL; J02600; AAA41596.1; -;
 CC PIR; A31890; A31890.
 CC HSP; P02760; LB1K.
 CC InterPro; IPR002223; Kunitz_BPTI.
 CC InterPro; IPR002345; Lipocalin.
 CC Pfam; PF000566; Lipocalin_cytfabp.
 CC Pfam; PF00014; Kunitz_BPTI; 2.
 CC Pfam; PF00061; Lipocalin; 1.
 CC PRINTS; PR00759; BASICPTASE.
 CC PRINTS; PR001179; LIPOCALIN.
 CC SMART; SM00131; K0; 2.
 CC PROSITE; PS00280; BPTI_KUNITZ_1; 2.
 CC PROSITE; PS00279; BPTI_KUNITZ_2; 2.
 CC PROSITE; PS00213; LIPOCALIN; 1.
 CC Glycoprotein; Plasma; Signal; Serine protease inhibitor; Repeat;
 KW Lipocalin.
 FT SIGNAL 1 19 BY SIMILARITY.
 FT CHAIN 20 202 ALPHA-1-MICROGLOBULIN.
 FT CHAIN 205 349 INTER-ALPHA-TRYPsin INHIBITOR LIGHT
 FT CHAIN
 FT CHAIN 283 343 TRYPSSTATIN.
 FT DOMAIN 230 280 BPTI/KUNITZ INHIBITOR 1.
 FT DOMAIN 286 336 BPTI/KUNITZ INHIBITOR 2.
 FT BINDING 52 52 CHROMOPHORE (BY SIMILARITY).
 FT

FT DISULFID 90 187 BY SIMILARITY.
 FT DISULFID 230 280 BY SIMILARITY.
 FT DISULFID 239 263 BY SIMILARITY.
 FT DISULFID 255 276 BY SIMILARITY.
 FT DISULFID 286 336 BY SIMILARITY.
 FT DISULFID 295 319 BY SIMILARITY.
 FT DISULFID 311 332 BY SIMILARITY.
 FT CARBOHYD 114 114 N-LINKED (GLCNAC...) (POTENTIAL).
 FT CARBOHYD 233 233 N-LINKED (GLCNAC...) (POTENTIAL).
 FT ACT_SITE 240 241 INHIBITORY SITE (P1) (CHYMOTRYPSIN,
 FT ELASTASE) (BY SIMILARITY).
 FT ACT_SITE 296 297 INHIBITORY SITE (P1) (TRYPSIN) (BY
 FT SIMILARITY).
 FT CONFLICT 142 142 G -> A (IN REF. 2).
 FT CONFLICT 302 302 W -> L (IN REF. 3).
 FT CONFLICT 323 323 G -> N (IN REF. 3).
 FT CONFLICT 330 331 KE -> PK (IN REF. 3).
 FT CONFLICT 334 334 E -> W (IN REF. 3).
 SQ SEQUENCE 349 AA; 38851 MW; 1B7FB7DCB0824E01 CRC64;
 Query Match 25.1%; Score 237.5; DB 1; Length 349;
 Best Local Similarity 30.4%; Pred.No. 1.8e-15;
 Matches 45; Conservative 17; Mismatches 47; Indels 39; Gaps 1;
 QY 9 DFCLVSKVYVGRCSNPMRWYNTDGSQOLFVYGGDGNNSNYLTKECKKCAVTENA 68
 DB 228 DSCOLNYSSEGPLGQQKYYNGASMACETFOYGCLGNNGNFASEKELQTCRTIAA-- 285
 QY 69 TGDLSATRNAADSSVPSAPRRDSDHSDMFENYECYTANAVTGPCRASFPWFYDVER 128
 DB 286 -----CNLPVQGPCRAFAELWAFDAQAQ 308
 QY 129 NSCNFNFIYGGCRGNKNSYRSEACMLRC 156
 DB 309 GKCIQFIYGGCKGNKGFYSECKEYIC 336
 RESULT 15
 TFPI_MACMU STANDARD; PRT; 304 AA.
 AC Q28864;
 DT 15-JUL-1999 (Rel. 38, Created)
 DT 15-JUL-1999 (Rel. 38, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Tissue factor pathway inhibitor precursor (TFPI) (Lipoprotein-
 DE associated coagulation inhibitor) (LACI) (Extrinsic pathway inhibitor)
 DE (EPI).
 GN TFPI OR TFPII.
 OS Macaca mulatta (Rhesus macaque).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
 OC Cercopithecoidea; Macaca.
 OX NCBI_TaxID=9544;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Liver.
 RX MEDLINE=94375417; PubMed=8089087;
 RA Kamei S., Kamikubo Y., Hamuro T., Fujimoto H., Ishihara M.,
 RA Ionomura H., Miyamoto S., Funatsu A., Enyoji K., Abumiya T.;
 RT "Amino acid sequence and inhibitory activity of rhesus monkey tissue
 RT factor pathway inhibitor (TFPI): comparison with human TFPI.";
 RL J. Biochem. 115:708-714(1994).
 CC -!- FUNCTION: INHIBITS FACTOR X (X(A)) DIRECTLY AND, IN A XA-DEPENDENT
 CC WAY, INHIBITS VII(A)/TISSUE FACTOR ACTIVITY, PRESUMABLY BY FORMING
 CC A QUATERNARY X(A)/LACI/VII(A)/TF COMPLEX. IT POSSESSES AN
 CC ANTITHROMBOTIC ACTION AND ALSO THE ABILITY TO ASSOCIATE WITH
 CC LIPOPROTEINS IN PLASMA.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- DOMAIN: THIS INHIBITOR CONTAINS THREE INHIBITORY DOMAINS.
 CC -!- PTM: O-GLYCOSYLATED (BY SIMILARITY).
 CC -!- SIMILARITY: CONTAINS 3 BPTI/KUNITZ INHIBITOR DOMAINS.
 CC
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DR EMBL; S73337; AAB31955.1; -
DR HSP; P10646; ITFX.
DR InterPro; IPR002223; Kunitz_BPTI.
DR Pfam; PF00014; Kunitz_BPTI; 3.
DR PRINTS; PR00759; BASICPTASE.
DR SMART; SM00131; KU; 3.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 3.
DR PROSITE; PS0279; BPTI_KUNITZ_2; 3.
KW Serine protease inhibitor; Glycoprotein; Repeat; Blood coagulation;
KW Signal.
FT SIGNAL 1 28 BY SIMILARITY.
FT CHAIN 29 304 TISSUE FACTOR PATHWAY INHIBITOR.
FT DOMAIN 54 104 BPTI/KUNITZ INHIBITOR 1
FT (VII(A)/TISSUE FACTOR BINDING SITE).
FT BPTI/KUNITZ INHIBITOR 2
FT BPTI/KUNITZ INHIBITOR 3.
FT (FACTOR X(A) BINDING SITE).
FT BPTI/KUNITZ INHIBITOR 3.
FT BY SIMILARITY.
FT DISULFID 54 104 BY SIMILARITY.
FT DISULFID 63 87 BY SIMILARITY.
FT DISULFID 79 100 BY SIMILARITY.
FT ACT_SITE 64 65 REACTIVE BOND (BY SIMILARITY).
FT DISULFID 125 175 BY SIMILARITY.
FT DISULFID 134 158 BY SIMILARITY.
FT DISULFID 150 171 BY SIMILARITY.
FT ACT_SITE 135 136 REACTIVE BOND (BY SIMILARITY).
FT DISULFID 217 267 BY SIMILARITY.
FT DISULFID 226 250 BY SIMILARITY.
FT DISULFID 242 263 BY SIMILARITY.
FT ACT_SITE 227 228 REACTIVE BOND (BY SIMILARITY).
FT CARBOHYD 145 145 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 195 195 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 256 256 N-LINKED (GLCNAC. .) (POTENTIAL).
SQ SEQUENCE 304 AA; 35085 MW; 56E13B3FF16282B0 CRC64;

Query Match 24.9%; Score 236.5; DB 1; Length 304;
Best Local Similarity 34.9%; Pred. No. 2e-15;
Matches 53; Conservative 24; Mismatches 64; Indels 11; Gaps 4;
QY 9 DFCLSVKVGRCRASPWWYNTDSCOLFVYGGCDGNSNNVLTKEECLKKCATVTENA 68
Db 123 DFCFLEDPGICRGYTRIFYNNQSKQCFKYGCGLGNNNFETLECKNTC---EDGL 179
QY 69 TG----DLATSRNADSSVPSAPRQDSHSDMFNYYEYCTANAVTGPCRASFPWWYF 124
Db 180 NGFQVDNYGTQLNAVNS--QTP--QSTKVPSPFFPHGSPWCLAPADRGLCRANENRFY 235
QY 125 DVERNSCNNFIYGGCRGNKNSYRSEACMLRC 156
Db 236 NSVIGKCRPFKYGSGCGGNENNFTSKRECLRAC 267

Search completed: October 18, 2002, 10:34:09
Job time : 13 secs

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OM protein - protein search, using sw model

Run on: October 18, 2002, 10:33:48 ; Search time 17 Seconds
(without alignments)
960.893 Million cell updates/sec

Title: US-09-218-913D-52
Perfect score: 948
Sequence: 1 ADERSIHDFCLVSKVGVRC.....ACMLRCFROENPLPLGSK 170

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283138 seqs, 96089334 residues

Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_71.*
1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	658	69.4	252	2 JG0185	hepatocyte growth
2	250.5	26.4	1558	2 C89114	protein C37C3.6a
3	250.5	26.4	2167	2 T34395	hypothetical prote
4	249.5	26.3	352	1 TI001	alpha-1-microglobu
5	246.5	26.0	302	1 TI001	tissue factor path
6	244.5	25.8	123	2 A29652	inter-alpha-trypsi
7	244.5	25.8	352	1 HCU	alpha-1-microglobu
8	244	25.7	299	2 I46937	tissue factor path
9	243	25.6	300	2 S12143	lipoprotein-associ
10	242.5	25.6	337	1 TI001	alpha-1-microglobu
11	241.5	25.5	125	1 TI001	alpha-1-microglobu
12	240	25.3	2225	2 T26063	hypothetical prote
13	239.5	25.3	396	2 S53325	tissue factor path
14	237.5	25.1	349	2 S21089	alpha-1-microglobu
15	236.5	24.9	304	1 JC2264	tissue factor path
16	235.5	24.8	349	2 S35708	alpha-1-microglobu
17	233.5	24.6	304	1 TI001	tissue factor path
18	222	23.4	1043	2 T19734	hypothetical prote
19	219	23.1	922	2 T23573	hypothetical prote
20	214.5	22.6	235	2 A54951	tissue factor path
21	210	22.2	765	2 S42880	amyloid precursor
22	209	22.0	1743	2 T26859	hypothetical prote
23	208	21.9	751	2 A49974	beta-amyloid precu
24	200	21.1	763	2 A49321	amyloid beta (A4)
25	200	21.1	1599	2 T16210	hypothetical prote
26	199	21.0	1522	2 H88380	protein T22F7.3 [1
27	195	20.6	1391	2 S41082	hypothetical prote
28	193.5	20.4	111	2 S41082	amyloid precursor
29	193	20.4	1474	2 D88550	protein ZC84.6 [1m

30	193	20.4	2844	2 S28291	hypothetical prote
31	191	20.1	1416	2 E88550	protein ZC84.1 [1m
32	186.5	19.7	747	2 JH0773	Alzheimer's diseas
33	186	19.6	484	4 A32761	hypothetical Alzhe
34	186	19.6	770	1 QRH044	Alzheimer's diseas
35	185.5	19.6	1203	2 T21275	hypothetical prote
36	181.5	19.1	355	1 S22181	gamma-1-microglobu
37	178	18.8	1965	2 T33216	hypothetical prote
38	175.5	18.5	76	2 S03607	Alzheimer's diseas
39	174.5	18.4	76	2 S04855	Alzheimer's diseas
40	174.5	18.4	76	2 S06678	Alzheimer's diseas
41	174.5	18.4	100	2 A32282	Alzheimer's diseas
42	174.5	18.4	692	2 T32980	hypothetical prote
43	167	17.6	62	2 S07451	proteinase inhibit
44	164	17.3	838	2 T20125	hypothetical prote
45	163.5	17.2	372	2 JC2556	alpha-1-microglobu

ALIGNMENTS

RESULT 1

JG0185
hepatocyte growth factor activator inhibitor type 2 - mouse
C:Species: Mus musculus (house mouse)
C:Date: 23-Jul-1999 #sequence_revision 23-Jul-1999 #text_change 11-May-2000
C:Accession: JG0185
R:Ittoh, H.; Kataoka, H.; Hamasuna, R.; Kitamura, N.; Kono, M.
Biochem. Biophys. Res. Commun. 255, 740-748, 1999
A:Title: Hepatocyte growth factor activator inhibitor type 2 lacking the first kunitz
A:Reference number: JG0185; MUID:99160423
A:Accession: JG0185
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-252 <ITO>
A:Cross-references: GB:AF099016
C:Superfamily: animal Kunitz-type proteinase inhibitor homology
F:133-183/Domain: animal Kunitz-type proteinase inhibitor homology <BPI>

Query Match 69.4%; Score 658; DB 2; Length 252;
Best Local Similarity 68.2%; Pred. No. 9.6e-52;
Matches 116; Conservative 20; Mismatches 34; Indels 0; Gaps 0;

QY	1	ADERSIHDFCLVSKVGVRCASMPRWYNTDSCOLFVYGGDGNNNYLTKEECLKK	60
DB	28	ASRELDVHESCGYKVVGKCRASIPRWYNTDSCOLFVYGGDGNNNYQSKEECLKD	87
QY	61	CATVTENATGDLATSRNAADSSVPSAPRRQDSEHDHSMFNEYCYTANAVTGPCRASFP	120
DB	88	CAGVTENTDDNARNRGADSSVLSVPRKQSAEDLSAEIENYECVPAKVTGCPRAAFP	147
QY	121	RWYFDVERNSCNFIYGGCGKNSYRSEACMLRCFROENPLPLGSK	170
DB	148	RWYDTEKNKSCISFIYGGCGKNSYLSQACMHCQKQMHPLPLGPK	197

RESULT 2

C89114
protein C37C3.6a [Imported] - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 10-May-2001
C:Accession: C89114
R:anonymous, The C. elegans Sequencing Consortium.
Science 282, 2012-2018, 1998
A:Title: Genome sequence of the nematode C. elegans: a platform for investigating bio
A:Reference number: A75000; MUID:99069613; PMID:9851916
A:Note: see webistes genome.wustl.edu/gsc/C.elegans/ and www.sanger.ac.uk/Projects/C-
A:Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999;
A:Accession: C89114
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-1558 <STO>
A:Cross-references: GB:chr_v; PIDN:AAC25867.1; PID:g3294501; GSPDB:GN00023; CESP:C37C

A:Molecule type: protein
A:Residues: 20-24 <CAL2>
R:Bourguignon, J.; Diarra-Mehrpour, M.; Sesboue, R.; Frain, M.; Sala-Trepat, J.M.; Ma Biochem. Biophys. Res. Commun. 131, 1146-1153, 1985
A>Title: Human inter-alpha-trypsin-inhibitor: characterization and partial nucleotide A:Reference number: I52208; MUID:86025577
A:Accession: I52208
A>Status: translated from GB/EMBL/DDBJ
A:Molecule type: mRNA
A:Residues: 302-352 <BOU>
A:Cross-references: GB:M11562; NID:gl86587; PIDN:AAA59194.1; PID:g307077
R:Wojcik, E.G.C.; van den Berg, M.; van der Linden, I.K.; Poort, S.R.; Cupers, R.; Be Biochem. J. 311, 753-759, 1995
A>Title: Factor IX Zuthphen: a Cys(18) -> Arg mutation results in formation of a heter A:Reference number: S59509; MUID:96067589
A:Accession: S59509
A:Molecule type: protein
A:Residues: 27-35,'Y',37 <WOJ>
R:Atmani, F.; Mizon, J.; Khan, S.R.
Eur. J. Biochem. 236, 984-990, 1996
A>Title: Identification of uronic-acid-rich protein as urinary bikunin, the light cha A:Reference number: S66434; MUID:96270753
A:Accession: S66434
A:Molecule type: protein
A:Residues: 206-214,'X',216-230 <ATM2>
R:Akerstroem, B.; Bratt, T.; Enghild, J.J.
FEBS Lett. 362, 50-54, 1995
A>Title: Formation of the alpha(1)-microglobulin chromophore in mammalian and insect A:Reference number: S68728; MUID:95212582
A:Accession: S68728
A:Molecule type: protein
A:Residues: 89-100 <AKE>
R:Jessen, T.E.; Faarvang, K.L.; Ploug, M.
FEBS Lett. 230, 195-200, 1988
A>Title: Carbohydrate as covalent crosslink in human inter-alpha-trypsin inhibitor: a A:Reference number: S02431; MUID:88167187
A:Accession: S02431
A:Molecule type: protein
A:Residues: 206-214,'X',216-217 <JES>
R:Lopez, C.; Grubb, A.; Mendez, E.
FEBS Lett. 144, 349-353, 1982
A>Title: Human protein HC displays variability in its carboxyl-terminal amino acid se A:Reference number: A91304
A:Contents: annotation; variant of alpha-1-microglobulin
A>Note: pooled urine samples contained two forms of this protein, both lacking 57-Lys R:Hochstrasser, K.; Schonberger, O.L.; Rossmannith, I.; Wächter, E.
Hoppe-Seyler's Z. Physiol. Chem. 362, 1357-1362, 1981
A>Title: Kunitz-type proteinase inhibitors derived by limited proteolysis of the inte by affinity chromatography.
A:Reference number: A91698; MUID:82074265
A:Contents: annotation; carbohydrate binding sites
R:Morill, M.; Travis, J.
Biol. Chem. Hoppe-Seyler 366, 19-21, 1985
A>Title: The reactive site of human inter-alpha-trypsin inhibitor is in the amino-ter A:Reference number: A90682; MUID:85225940
A:Contents: annotation; inhibitory site
A>Note: in vitro, the first twelve residues of the amino end of the inhibitor appear wn
C:Comment: Alpha-1-microglobulin and inter-alpha-trypsin inhibitor are proteolyticall C:Comment: Alpha-1-microglobulin occurs in many physiological fluids including plasma . It contains at least one brown-yellow chromophore.

	Query Match	Best Local Similarity	Matches	Conservative	Indels	Gaps	Length
QY	9 DFLCVKVGRCRASPMRWNYNTDGSOLFVYGCGDGNSNNYLTKKECLKKCATTENA 68	25.8%; Score 244.5;	DB 1;	Length 352;			
Db	229 DSQLGVSAGPCMGMSRFYNGTSMACETFYQGCGMGNFNVEKECLQTCTVAA-- 286	32.4%; Pred. No. 1.6e-14;	Mismatches 14;	Indels 39;	Gaps 1;		
QY	69 TGDLSNRNAADSVSPAPROQSDHSSDMFNEEYCTANAVTGPCRASFPRMYFDVER 128						
Db	287 -----CNLPYVRGPCRAFIOLWAFDAVKVG309						

Best Local Similarity 30.0%; Pred. No.1.9e-14;
Matches 48; Conservative 23; Mismatches 61; Indels 28; Gaps 2;

QY 129 NSCNFFIYGGCGRGNKNSYRSEACMLRC 156
Db 310 GKCVLFYGGCGGNGNKFSEKEKREYC 337

RESULT 8
I46937
tissue factor pathway inhibitor - rabbit
C:Species: Oryctolagus cuniculus (domestic rabbit)
C:Date: 04-Sep-1997 #sequence_revision 04-Sep-1997 #text_change 13-Aug-1999
C:Accession: I46937
R:Belacouaj, A.; Kuppuswamy, M.N.; Birktoft, J.J.; Bajaj, S.P.
Thromb. Res. 69, 547-553, 1993
A:Title: Revised cDNA sequence of rabbit tissue factor pathway inhibitor.
A:Reference number: I46937; MUID:93276427
A:Accession: I46937
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-299 <BEL>
A:Cross-references: GB:S61902; NID:g386015; PIDN:AAB26836.1; PID:g386016
C:Superfamily: tissue factor pathway inhibitor; animal Kunitz-type proteinase inhibitor
F:49-99/Domain: animal Kunitz-type proteinase inhibitor homology <BPI>
F:120-170/Domain: animal Kunitz-type proteinase inhibitor homology <BPI>
F:212-262/Domain: animal Kunitz-type proteinase inhibitor homology <BPI2>

Query Match 25.7%; Score 244; DB 2; Length 299;
Best Local Similarity 30.0%; Pred. No.1.5e-14;
Matches 48; Conservative 23; Mismatches 61; Indels 28; Gaps 2;

QY 4 ERSIHDFCLVSKVVGRCRASMPPRWYNTDGSQCLFVYGGCGDNNSNYLTKECLKKCAT 63
Db 42 QKPTSHFCAMKVDGPRCAVYIKRFFENILHQCEEFYGGCGENRPFSELECKEKAR 102

QY 64 VTENATGDLATSRNAADSSVPSAPRRQDSHSDMFNIEEYCTANAVTGPCRASPRWY 123
Db 102 DYPKMTTKLTFQKGP-----FCFLEEDPGICRGYITRYF 137

QY 124 FDNVNSCNFFIYGGCGRGNKNSYRSEACMLRCFRQENP 163
Db 138 YNNQSKOCERFKYGGCLGNLNNFSELECKNTC-----ENP 173

RESULT 9
S12143
lipoprotein-associated coagulation inhibitor precursor - rabbit
N:Alternate names: endothelial cell coagulation inhibitor; endothelial cell tissue factor
C:Species: Oryctolagus cuniculus (domestic rabbit)
C:Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 16-Jul-1999
C:Accession: S12143; A61373
R:Wesselschmidt, R.L.; Girard, T.J.; Broze Jr., G.J.
Nucleic Acids Res. 18, 6440, 1990
A:Title: cDNA sequence of rabbit lipoprotein-associated coagulation inhibitor.
A:Reference number: S12143; MUID:91057146
A:Accession: S12143
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-300 <WES>
A:Cross-references: EMBL:X54708; NID:g1612; PIDN:CAA38515.1; PID:g1613
R:Colburn P.; Crabh J.W.; Buonassisi, V.
J. Cell. Physiol. 148, 320-326, 1991
A:Title: Enhanced inhibition of tissue factor by the extended form of an endothelial cell
A:Reference number: A61373; MUID:91349227
A:Accession: A61373
A:Molecule type: protein
A:Residues: 25-33, 'X', 35-46 <COL>
C:Superfamily: tissue factor pathway inhibitor; animal Kunitz-type proteinase inhibitor
F:50-100/Domain: animal Kunitz-type proteinase inhibitor homology <BPI>
F:121-171/Domain: animal Kunitz-type proteinase inhibitor homology <BPI2>
F:213-263/Domain: animal Kunitz-type proteinase inhibitor homology <BPI3>

Query Match 25.6%; Score 243; DB 2; Length 300;

QY 129 NSCNFFIYGGCGRGNKNSYRSEACMLRC 156
Db 310 GKCVLFYGGCGGNGNKFSEKEKREYC 337

RESULT 8
I46937
tissue factor pathway inhibitor - rabbit
C:Species: Oryctolagus cuniculus (domestic rabbit)
C:Date: 04-Sep-1997 #sequence_revision 04-Sep-1997 #text_change 13-Aug-1999
C:Accession: I46937
R:Belacouaj, A.; Kuppuswamy, M.N.; Birktoft, J.J.; Bajaj, S.P.
Thromb. Res. 69, 547-553, 1993
A:Title: Revised cDNA sequence of rabbit tissue factor pathway inhibitor.
A:Reference number: I46937; MUID:93276427
A:Accession: I46937
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-299 <BEL>
A:Cross-references: GB:S61902; NID:g386015; PIDN:AAB26836.1; PID:g386016
C:Superfamily: tissue factor pathway inhibitor; animal Kunitz-type proteinase inhibitor
F:49-99/Domain: animal Kunitz-type proteinase inhibitor homology <BPI>
F:120-170/Domain: animal Kunitz-type proteinase inhibitor homology <BPI>
F:212-262/Domain: animal Kunitz-type proteinase inhibitor homology <BPI2>

Query Match 25.7%; Score 244; DB 2; Length 299;
Best Local Similarity 30.0%; Pred. No.1.5e-14;
Matches 48; Conservative 23; Mismatches 61; Indels 28; Gaps 2;

QY 4 ERSIHDFCLVSKVVGRCRASMPPRWYNTDGSQCLFVYGGCGDNNSNYLTKECLKKCAT 63
Db 42 QKPTSHFCAMKVDGPRCAVYIKRFFENILHQCEEFYGGCGENRPFSELECKEKAR 102

QY 64 VTENATGDLATSRNAADSSVPSAPRRQDSHSDMFNIEEYCTANAVTGPCRASPRWY 123
Db 102 DYPKMTTKLTFQKGP-----FCFLEEDPGICRGYITRYF 137

QY 124 FDNVNSCNFFIYGGCGRGNKNSYRSEACMLRCFRQENP 163
Db 138 YNNQSKOCERFKYGGCLGNLNNFSELECKNTC-----ENP 173

RESULT 9
S12143
lipoprotein-associated coagulation inhibitor precursor - rabbit
N:Alternate names: endothelial cell coagulation inhibitor; endothelial cell tissue factor
C:Species: Oryctolagus cuniculus (domestic rabbit)
C:Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 16-Jul-1999
C:Accession: S12143; A61373
R:Wesselschmidt, R.L.; Girard, T.J.; Broze Jr., G.J.
Nucleic Acids Res. 18, 6440, 1990
A:Title: cDNA sequence of rabbit lipoprotein-associated coagulation inhibitor.
A:Reference number: S12143; MUID:91057146
A:Accession: S12143
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-300 <WES>
A:Cross-references: EMBL:X54708; NID:g1612; PIDN:CAA38515.1; PID:g1613
R:Colburn P.; Crabh J.W.; Buonassisi, V.
J. Cell. Physiol. 148, 320-326, 1991
A:Title: Enhanced inhibition of tissue factor by the extended form of an endothelial cell
A:Reference number: A61373; MUID:91349227
A:Accession: A61373
A:Molecule type: protein
A:Residues: 25-33, 'X', 35-46 <COL>
C:Superfamily: tissue factor pathway inhibitor; animal Kunitz-type proteinase inhibitor
F:50-100/Domain: animal Kunitz-type proteinase inhibitor homology <BPI>
F:121-171/Domain: animal Kunitz-type proteinase inhibitor homology <BPI2>
F:213-263/Domain: animal Kunitz-type proteinase inhibitor homology <BPI3>

Query Match 25.6%; Score 243; DB 2; Length 300;

QY 129 NSCNFFIYGGCGRGNKNSYRSEACMLRC 156
Db 310 GKCVLFYGGCGGNGNKFSEKEKREYC 337

RESULT 8
I46937
tissue factor pathway inhibitor - rabbit
C:Species: Oryctolagus cuniculus (domestic rabbit)
C:Date: 04-Sep-1997 #sequence_revision 04-Sep-1997 #text_change 13-Aug-1999
C:Accession: I46937
R:Belacouaj, A.; Kuppuswamy, M.N.; Birktoft, J.J.; Bajaj, S.P.
Thromb. Res. 69, 547-553, 1993
A:Title: Revised cDNA sequence of rabbit tissue factor pathway inhibitor.
A:Reference number: I46937; MUID:93276427
A:Accession: I46937
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-299 <BEL>
A:Cross-references: GB:S61902; NID:g386015; PIDN:AAB26836.1; PID:g386016
C:Superfamily: tissue factor pathway inhibitor; animal Kunitz-type proteinase inhibitor
F:49-99/Domain: animal Kunitz-type proteinase inhibitor homology <BPI>
F:120-170/Domain: animal Kunitz-type proteinase inhibitor homology <BPI>
F:212-262/Domain: animal Kunitz-type proteinase inhibitor homology <BPI2>

Query Match 25.7%; Score 244; DB 2; Length 299;
Best Local Similarity 30.0%; Pred. No.1.5e-14;
Matches 48; Conservative 23; Mismatches 61; Indels 28; Gaps 2;

QY 4 ERSIHDFCLVSKVVGRCRASMPPRWYNTDGSQCLFVYGGCGDNNSNYLTKECLKKCAT 63
Db 42 QKPTSHFCAMKVDGPRCAVYIKRFFENILHQCEEFYGGCGENRPFSELECKEKAR 102

QY 64 VTENATGDLATSRNAADSSVPSAPRRQDSHSDMFNIEEYCTANAVTGPCRASPRWY 123
Db 102 DYPKMTTKLTFQKGP-----FCFLEEDPGICRGYITRYF 137

QY 124 FDNVNSCNFFIYGGCGRGNKNSYRSEACMLRCFRQENP 163
Db 138 YNNQSKOCERFKYGGCLGNLNNFSELECKNTC-----ENP 173

RESULT 9
S12143
lipoprotein-associated coagulation inhibitor precursor - rabbit
N:Alternate names: endothelial cell coagulation inhibitor; endothelial cell tissue factor
C:Species: Oryctolagus cuniculus (domestic rabbit)
C:Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 16-Jul-1999
C:Accession: S12143; A61373
R:Wesselschmidt, R.L.; Girard, T.J.; Broze Jr., G.J.
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A:Title: cDNA sequence of rabbit lipoprotein-associated coagulation inhibitor.
A:Reference number: S12143; MUID:91057146
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A:Status: preliminary
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A:Residues: 1-300 <WES>
A:Cross-references: EMBL:X54708; NID:g1612; PIDN:CAA38515.1; PID:g1613
R:Colburn P.; Crabh J.W.; Buonassisi, V.
J. Cell. Physiol. 148, 320-326, 1991
A:Title: Enhanced inhibition of tissue factor by the extended form of an endothelial cell
A:Reference number: A61373; MUID:91349227
A:Accession: A61373
A:Molecule

Query Match	Score 243;	DB 2;	Length 300;
25.6%;	Score 243;	DB 2;	Length 300;
QY	69	TGDLATSRNAADSSVPSAPRRQDSHSSDMFVEEYCTANAVTGCGRASPRWTFDVER	128

[illegible]

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: October 18, 2002, 10:33:48 ; Search time 32 Seconds
(without alignments)
590.080 Million cell updates/sec

Title: US-09-218-913D-52

Perfect score: 948

Sequence: 1 ADDRESSIHDFCLVSKVGRG.....ACMLRCFRQENPPLPLGSK 170

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 747574 seqs, 111073796 residues

Total number of hits satisfying chosen parameters: 747574

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	ID	Description
1	948	100.0	170	18 AAW30041	Human placental bi
2	948	100.0	170	21 AAB14189	Human placental bi
3	948	100.0	170	21 AAB14190	Human placental bi
4	948	100.0	179	18 AAW30053	Human placental bi
5	948	100.0	179	21 AAB14159	Mature human place
6	948	100.0	197	18 AAW30043	Human placental bi
7	948	100.0	197	21 AAB14160	Human placental bi
8	948	100.0	213	18 AAW30042	Human placental bi
9	948	100.0	213	21 AAB14184	Human placental bi
10	948	100.0	213	21 AAB14200	Human placental bi
11	948	100.0	225	18 AAW30046	Human placental bi

12	948	100.0	225	21 AAB14186	Human placental bi
13	948	100.0	225	21 AAB14201	Human placental bi
14	948	100.0	235	18 AAW30060	Human consensu bi
15	948	100.0	235	21 AAB14167	Human placental bi
16	948	100.0	240	18 AAW30045	Human placental bi
17	948	100.0	248	18 AAW30044	Human consensu bi
18	948	100.0	248	21 AAB14183	Human placental bi
19	948	100.0	252	18 AAW30040	Human placental bi
20	948	100.0	252	19 AAW13665	Hepatocyte growth
21	948	100.0	252	18 AAW70286	Human tissue facto
22	948	100.0	252	21 AAB14187	Human placental bi
23	948	100.0	259	21 AAB14207	Human placental bi
24	948	100.0	289	21 AAB43821	Human cancer assoc
25	945	99.7	240	21 AAB14185	Human placental bi
26	945	99.7	252	22 ABB50286	Kunitz type 2 Ser
27	859	90.6	153	18 AAW30051	Human placental bi
28	859	90.6	153	21 AAB14161	Human placental bi
29	819	86.4	146	18 AAW30052	Human placental bi
30	819	86.4	146	21 AAB14188	Human consensu bi
31	750	79.1	170	18 AAW30061	Human placental bi
32	750	79.1	179	21 AAB14168	Human placental bi
33	501	52.8	92	18 AAW30054	Human placental bi
34	501	52.8	92	21 AAB14166	Human placental bi
35	490	51.7	130	21 AAB14169	Human placental bi
36	488	51.5	130	18 AAW30062	EST R35464 protein
37	487	51.4	169	18 AAW30063	EST R74593 protein
38	487	51.4	169	21 AAB14170	Human placental bi
39	337	35.5	58	18 AAW30049	Human placental bi
40	337	35.5	58	21 AAB14164	Human placental bi
41	334	35.2	58	18 AAW30047	Human placental bi
42	334	35.2	58	21 AAB14162	Human placental bi
43	312	32.9	513	18 AAW27368	Hepatocyte growth
44	312	32.9	513	20 AAW92653	Human HAI-1 protei
45	312	32.9	513	21 AAB19553	Human hepatocyte g

ALIGNMENTS

RESULT 1
AAW30041
ID AAW30041 standard; Protein; 170 AA.
XX
AC AAW30041;
XX
DT 20-APR-1998 (first entry)
XX
DE Human placental bikunin.
XX
DE Human; placental bikunin; inhibition; trypsin; kallikrein;
KW plasmin; factor xIIa; treatment; prevention; oedema;
KW inflammation; infection; granulomatosis; multiple sclerosis;
KW ischaemia; perioperative blood loss; sepsis; shock; fibrosis;
KW blood coagulation disease; polytrauma; stroke; haemorrhage;
KW gastric cancer; cervical cancer; metastasis; blood loss.
XX
OS Homo sapiens.
XX
PN WO9733996-A2.
XX
PD 18-SEP-1997.
XX
PF 10-MAR-1997; 97WO-US03894.
XX
PR 04-OCT-1996; 96US-0725251.
PR 11-MAR-1996; 96US-0013106.
PR 14-JUN-1996; 96US-0019793.
XX
PA (FARB) BAYER CORP.
XX
PI Davis G, Delaria KA, Marlor CW, Muller DK, Tamburini PP;
XX WPI; 1997-470876/43.
DR

XX New human placental bikunin - used to inhibit kallikrein, trypsin
 PT etc. in treatment of oedema, multiple sclerosis, fibrosis, or
 PT perioperative blood loss
 XX
 PS Claim 1: Page 65; 110pp; English.
 XX
 CC The present sequence is a human placental bikunin, which
 CC inhibits, e.g. trypsin, kallikrein, plasmin and factor XIIa.
 CC Bikunin can be used to treat or prevent brain and spinal cord
 CC oedema, inflammation, infection or granulomatosis, multiple
 CC sclerosis, ischaemia, perioperative blood loss, sepsis, shock,
 CC fibrosis, blood coagulation diseases, polytrauma, stroke,
 CC cerebral or subarachnoid haemorrhage and gastric or cervical
 CC cancer and prevent metastasis. It is particularly useful for
 CC reducing blood loss during surgery, and can also be used to treat
 CC other cancer, arthritis, anaemia, non-insulin dependent diabetes,
 CC influenza and similar viral infections, acute pancreatitis and
 CC gout, and prevent pre-term labour. It has similar properties to
 CC aprotinin, but is less highly charged so should be less
 CC immunogenic and less likely to damage the kidneys. Manipulation
 CC of the bikunin sequence may allow the inhibitory profile to be
 CC altered. It also reduces or eliminates the need for whole donor
 CC blood or blood products during surgery, thereby reducing the risk
 CC of infection and other adverse side effects, as well as reducing
 CC the cost of surgery.
 XX
 SQ Sequence 170 AA;
 Query Match 100.0%; Score 948; DB 18; Length 170;
 Best Local Similarity 100.0%; Pred. No. 4e-89;
 Matches 170; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ADERSIHDFCLVSKVVGRCRAMPWWYNTDGSQCLFVYGGCDGNSNNYLTKECLKK 60
 DB 1 ADERSIHDFCLVSKVVGRCRAMPWWYNTDGSQCLFVYGGCDGNSNNYLTKECLKK 60
 QY 61 CATVTENATGDLATSRNAADSSVPSAPRRQDSHSDMFNVEEYCTANAVTGPCRASFP 120
 DB 61 CATVTENATGDLATSRNAADSSVPSAPRRQDSHSDMFNVEEYCTANAVTGPCRASFP 120
 QY 121 RWYFDVERNSCNFIYGGCRGNKNSYRSEACMLRCFROQENPPLPLGSK 170
 DB 121 RWYFDVERNSCNFIYGGCRGNKNSYRSEACMLRCFROQENPPLPLGSK 170
 RESULT 2
 AAB14189
 ID AAB14189 standard; protein; 170 AA.
 AC AAB14189;
 DT 02-FEB-2001 (first entry)
 XX Human placental bikunin protein # 7.
 DE Human; mucociliary dysfunction; mucus; sputum;
 KW chronic obstructive lung disease; chronic bronchitis; CB; Bronchiectasis;
 KW BE; asthma; cystic fibrosis; CF; bacterial infection; placental bikunin;
 KW Kunitz-type serine protease inhibitor; chronic sinusitis; glue ear.
 XX
 OS Homo sapiens.
 XX
 XX WO200037099-A2.
 XX 29-JUN-2000.
 XX 22-DEC-1999; 99WO-GB04381.
 XX 22-DEC-1998; 98US-0218913.
 XX 17-NOV-1999; 99US-0441966.
 XX (FARB) BAYER AG.

XX Hall R, Poll CT, Newton BB, Taylor WJA;
 XX WPI; 2000-452127/39.
 XX
 PT Stimulating mucociliary clearance rate of mucus and sputum in lung
 PT airways for treating lung diseases such as cystic fibrosis and
 PT bronchitis involves administering a Kunitz-type serine protease
 PT inhibitor -
 XX
 PS Disclosure; Pages 166-167; 173pp; English.
 XX
 CC Mucociliary dysfunction is the inability of ciliated epithelium to clear
 CC mucus and sputum in lung airways. Mucociliary dysfunction is a serious
 CC complication of chronic obstructive lung diseases such as Chronic
 CC Bronchitis (CB), Bronchiectasis (BE), asthma and Cystic Fibrosis (CF).
 CC In addition, patients suffering from mucociliary dysfunction are
 CC susceptible to secondary bacterial infections. The present sequence is
 CC a sequence for human placental bikunin protein. This sequence was
 CC derived from a human placental cDNA library by PCR-based amplification.
 CC This protein is a Kunitz-type serine protease inhibitor protein, which
 CC can stimulate the rate of mucociliary clearance of mucus and sputum in
 CC lung airways. Therefore, the present protein may be used for treating
 CC lung diseases such as CF, CB, BE, and chronic sinusitis and glue ear
 CC which are caused by retention and accumulation of mucus.
 CC Note: the present sequence is defined as SEQ ID 51 in the sequence
 CC listing. However, in figure 4C of the specification, SEQ ID 51 is
 CC clearly shown as a nucleotide sequence. Therefore, the nucleotide
 CC sequence has been described in AAA70392.
 XX
 SQ Sequence 170 AA;
 Query Match 100.0%; Score 948; DB 21; Length 170;
 Best Local Similarity 100.0%; Pred. No. 4e-89;
 Matches 170; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ADERSIHDFCLVSKVVGRCRAMPWWYNTDGSQCLFVYGGCDGNSNNYLTKECLKK 60
 DB 1 ADERSIHDFCLVSKVVGRCRAMPWWYNTDGSQCLFVYGGCDGNSNNYLTKECLKK 60
 QY 61 CATVTENATGDLATSRNAADSSVPSAPRRQDSHSDMFNVEEYCTANAVTGPCRASFP 120
 DB 61 CATVTENATGDLATSRNAADSSVPSAPRRQDSHSDMFNVEEYCTANAVTGPCRASFP 120
 QY 121 RWYFDVERNSCNFIYGGCRGNKNSYRSEACMLRCFROQENPPLPLGSK 170
 DB 121 RWYFDVERNSCNFIYGGCRGNKNSYRSEACMLRCFROQENPPLPLGSK 170
 RESULT 3
 AAB14190
 ID AAB14190 standard; protein; 170 AA.
 AC AAB14190;
 DT 02-FEB-2001 (first entry)
 XX Human placental bikunin protein # 8.
 DE Human; mucociliary dysfunction; mucus; sputum;
 KW chronic obstructive lung disease; chronic bronchitis; CB; Bronchiectasis;
 KW BE; asthma; cystic fibrosis; CF; bacterial infection; placental bikunin;
 KW Kunitz-type serine protease inhibitor; chronic sinusitis; glue ear.
 XX
 OS Homo sapiens.
 XX
 XX WO200037099-A2.
 XX 29-JUN-2000.
 XX 22-DEC-1999; 99WO-GB04381.
 XX 22-DEC-1998; 98US-0218913.
 XX 17-NOV-1999; 99US-0441966.
 XX (FARB) BAYER AG.

PR 17-NOV-1999; 99US-0441966.
XX (FARB) BAYER AG.
XX PI Hall R, Poll CT, Newton BB, Taylor WJA;
XX DR WPI; 2000-452127/39.
XX
XX Stimulating mucociliary clearance rate of mucus and sputum in lung
PT airways for treating lung diseases such as cystic fibrosis and
PT bronchitis involves administering a Kunitz-type serine protease
PT inhibitor
XX
XX Claim 14; Page 90; 173pp; English.
XX
XX Mucociliary dysfunction is the inability of ciliated epithelium to clear
CC mucus and sputum in lung airways. Mucociliary dysfunction is a serious
CC complication of chronic obstructive lung diseases such as Chronic
CC Bronchitis (CB), Bronchiectasis (BE), asthma and Cystic Fibrosis (CF).
CC In addition, patients suffering from mucociliary dysfunction are
CC susceptible to secondary bacterial infections. The present sequence is
CC a sequence for human placental bikunin protein. This sequence was derived
CC from a human placental cDNA library by PCR-based amplification. This
CC protein is a Kunitz-type serine protease inhibitor protein, which can
CC stimulate the rate of mucociliary clearance of mucus and sputum in lung
CC airways. Therefore, the present protein may be used for treating lung
CC diseases such as CF, CB, BE, and chronic sinusitis and glue ear which
CC are caused by retention and accumulation of mucus.
XX
XX Sequence 170 AA;
SQ
Query Match 100.0%; Score 948; DB 21; Length 170;
Best Local Similarity 100.0%; Pred. No. 4e-89;
Matches 170; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ADERSIHDFCLVSKVVGRCRASPMPRWYNTDGSQCLFVYGGDGNNSNYLTKEECLKK 60
Db 1 ADERSIHDFCLVSKVVGRCRASPMPRWYNTDGSQCLFVYGGDGNNSNYLTKEECLKK 60
QY 61 CATVTENATGDLATSRNAADSSVPSAPRRQDSEHSDMFNYYEYCTANAVTGPCRASFP 120
Db 61 CATVTENATGDLATSRNAADSSVPSAPRRQDSEHSDMFNYYEYCTANAVTGPCRASFP 120
QY 121 RWYFDVERNSCNNFIYGGCRGNKNSRSEACMLRCFROQENPPLPLGSK 170
Db 121 RWYFDVERNSCNNFIYGGCRGNKNSRSEACMLRCFROQENPPLPLGSK 170
RESULT 4
AAW30053
ID AAW30053 standard; Protein; 179 AA.
XX
XX AAW30053;
XX
XX 20-APR-1998 (first entry)
XX
XX Human placental bikunin.
XX
XX Human; placental bikunin; inhibition; trypsin; kallikrein;
KW plasmin; factor XIIa; treatment; prevention; oedema;
KW Inflammation; infection; granulomatosis; multiple sclerosis;
KW ischaemia; perioperative blood loss; sepsis; shock; fibrosis;
KW blood coagulation disease; polytrauma; stroke; haemorrhage;
KW gastric cancer; cervical cancer; metastasis; blood loss.
XX
XX Homo sapiens.
OS
XX
XX W09733996-A2.
PN
XX
XX 18-SEP-1997.
PD
XX
XX 10-MAR-1997; 97WO-US03894.
PF
XX

PR 04-OCT-1996; 96US-0725251.
PR 11-MAR-1996; 96US-0013106.
PR 14-JUN-1996; 96US-0019793.
XX
XX (FARB) BAYER CORP.
XX
XX Davis G, Delaria KA, Marlor CW, Muller DK, Tamburini PP;
XX PI
XX WPI; 1997-470876/43.
XX
XX New human placental bikunin - used to inhibit kallikrein, trypsin
PT etc. in treatment of oedema, multiple sclerosis, fibrosis, or
PT perioperative blood loss
XX
XX Claim 1; Page 67; 110pp; English.
PS
XX The present sequence is a human placental bikunin, which
XX inhibits, e.g. trypsin, kallikrein, plasmin and factor XIIa.
CC Bikunin can be used to treat or prevent brain and spinal cord
CC oedema, inflammation, infection or granulomatosis, multiple
CC sclerosis, ischaemia, perioperative blood loss, sepsis, shock,
CC fibrosis, blood coagulation diseases, polytrauma, stroke, cerebral
CC or subarachnoid haemorrhage and gastric or cervical
CC cancer and prevent metastasis. It is particularly useful for
CC reducing blood loss during surgery, and can also be used to treat
CC other cancer, arthritis, anaemia, non-insulin dependent diabetes,
CC influenza and similar viral infections, acute pancreatitis and
CC gout, and prevent pre-term labour. It has similar properties to
CC aprotinin, but is less highly charged so should be less
CC immunogenic and less likely to damage the kidneys. Manipulation
CC of the bikunin sequence may allow the inhibitory profile to be
CC altered. It also reduces or eliminates the need for whole donor
CC blood or blood products during surgery, thereby reducing the risk
CC of infection and other adverse side effects, as well as reducing
CC the cost of surgery.
XX
XX Sequence 179 AA;
SQ
Query Match 100.0%; Score 948; DB 18; Length 179;
Best Local Similarity 100.0%; Pred. No. 4.2e-89;
Matches 170; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ADERSIHDFCLVSKVVGRCRASPMPRWYNTDGSQCLFVYGGDGNNSNYLTKEECLKK 60
Db 1 ADERSIHDFCLVSKVVGRCRASPMPRWYNTDGSQCLFVYGGDGNNSNYLTKEECLKK 60
QY 61 CATVTENATGDLATSRNAADSSVPSAPRRQDSEHSDMFNYYEYCTANAVTGPCRASFP 120
Db 61 CATVTENATGDLATSRNAADSSVPSAPRRQDSEHSDMFNYYEYCTANAVTGPCRASFP 120
QY 121 RWYFDVERNSCNNFIYGGCRGNKNSRSEACMLRCFROQENPPLPLGSK 170
Db 121 RWYFDVERNSCNNFIYGGCRGNKNSRSEACMLRCFROQENPPLPLGSK 170
RESULT 5
AAB14159
ID AAB14159 standard; protein; 179 AA.
XX
XX AAB14159;
XX
XX 02-FEB-2001 (first entry)
XX
XX Mature human placental bikunin protein.
XX
XX Human; mucociliary dysfunction; mucus; sputum;
KW chronic obstructive lung disease; chronic bronchitis; CB; Bronchiectasis;
KW BE; asthma; cystic fibrosis; CF; bacterial infection; placental bikunin;
KW Kunitz-type serine protease inhibitor; chronic sinusitis; glue ear.
XX
XX Homo sapiens.
OS
XX
XX W0200037099-A2.
PN

XX 29-JUN-2000.
 XX PD
 XX PF
 XX 22-DEC-1999; 99WO-GB04381.
 XX 22-DEC-1998; 98US-0218913.
 PR 17-NOV-1999; 99US-0441966.
 XX (FARB) BAYER AG.
 XX PI Hall R, Poll,CT, Newton BB, Taylor WJA;
 XX WPI; 2000-452127/39.
 XX Stimulating mucociliary clearance rate of mucus and sputum in lung
 PT airways for treating lung diseases such as cystic fibrosis and
 PT bronchitis involves administering a Kunitz-type serine protease
 PT inhibitor -
 XX Claim 14; Pages 89-90; 173pp; English.
 XX PS
 XX CC Mucociliary dysfunction is the inability of ciliated epithelium to clear
 CC mucus and sputum in lung airways. Mucociliary dysfunction is a serious
 CC complication of chronic obstructive lung diseases such as Chronic
 CC Bronchitis (CB), Bronchiectasis (BE), asthma and Cystic Fibrosis (CF).
 CC In addition, patients suffering from mucociliary dysfunction are
 CC susceptible to secondary bacterial infections. The present sequence is
 CC human placental bikunin. This protein is a Kunitz-type serine protease
 CC inhibitor protein, which can stimulate the rate of mucociliary clearance
 CC of mucus and sputum in lung airways. Therefore, the present protein may
 CC be used for treating lung diseases such as CF, CB, BE, and chronic
 CC sinusitis and glue ear which are caused by retention and accumulation of
 CC mucus. The present sequence is the mature human placental bikunin protein
 CC sequence.
 XX SQ Sequence 179 AA;
 Query Match 100.0%; Score 948; DB 21; Length 179;
 Best Local Similarity 100.0%; Pred. No. 4.2e-89;
 Matches 170; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ADERSIHDFCLVSKVVGRCRSMRWYNTDGSQQLFVYGGCDGNSNNYLTKECLKK 60
 DB 1 ADERSIHDFCLVSKVVGRCRSMRWYNTDGSQQLFVYGGCDGNSNNYLTKECLKK 60
 QY 61 CATVTENATGDLATSRNAADSSVPSAPRRQDSHSDMFNVEYCTANAVTGPCRASFP 120
 DB 61 CATVTENATGDLATSRNAADSSVPSAPRRQDSHSDMFNVEYCTANAVTGPCRASFP 120
 QY 121 RWYFDVERNSCNNFIYGGCRGNKNSYRSEACMLRCFRQENPPLPLGSK 170
 DB 121 RWYFDVERNSCNNFIYGGCRGNKNSYRSEACMLRCFRQENPPLPLGSK 170
 RESULT 6
 AAW30043
 ID AAW30043 standard; Protein; 197 AA.
 XX AC AAW30043;
 XX 20-APR-1998 (first entry)
 XX DE Human placental bikunin.
 XX Human; placental bikunin; inhibition; trypsin; kallikrein;
 KW plasmin; factor XIIa; treatment; prevention; oedema;
 KW inflammation; infection; granulomatosis; multiple sclerosis;
 KW ischaemia; perioperative blood loss; sepsis; shock; fibrosis;
 KW blood coagulation disease; polytrauma; stroke; haemorrhage;
 KW gastric cancer; cervical cancer; metastasis; blood loss.
 XX OS Homo sapiens.
 XX KW

PN WO9733996-A2.
 XX 18-SEP-1997.
 XX PF 10-MAR-1997; 97WO-US03894.
 XX 04-OCT-1996; 96US-0725251.
 PR 11-MAR-1996; 96US-0013106.
 PR 14-JUN-1996; 96US-0019793.
 XX (FARB) BAYER CORP.
 XX Davis G, Delaria KA, Marlor CW, Muller DK, Tamburini PP;
 XX WPI; 1997-470876/43.
 XX New human placental bikunin - used to inhibit kallikrein, trypsin
 PT etc. in treatment of oedema, multiple sclerosis, fibrosis, or
 PT perioperative blood loss
 XX Claim 1; Page 65; 110pp; English.
 XX The present sequence is a human placental bikunin, which
 CC inhibits, e.g. trypsin, kallikrein, plasmin and factor XIIa.
 CC Bikunin can be used to treat or prevent brain and spinal cord
 CC oedema, inflammation, infection or granulomatosis, multiple
 CC sclerosis, ischaemia, perioperative blood loss, sepsis, shock,
 CC fibrosis, blood coagulation diseases, polytrauma, stroke, cerebral
 CC or subarachnoid haemorrhage and gastric or cervical
 CC cancer and prevent metastasis. It is particularly useful for
 CC reducing blood loss during surgery, and can also be used to treat
 CC other cancer, arthritis, anaemia, non-insulin dependent diabetes,
 CC influenza and similar viral infections, acute pancreatitis and
 CC gout, and prevent pre-term labour. It has similar properties to
 CC aprotinin, but is less highly charged so should be less
 CC immunogenic and less likely to damage the kidneys. Manipulation
 CC of the bikunin sequence may allow the inhibitory profile to be
 CC altered. It also reduces or eliminates the need for whole donor
 CC blood or blood products during surgery, thereby reducing the risk
 CC of infection and other adverse side effects, as well as reducing
 CC the cost of surgery.
 XX SQ Sequence 197 AA;
 Query Match 100.0%; Score 948; DB 18; Length 197;
 Best Local Similarity 100.0%; Pred. No. 4.8e-89;
 Matches 170; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ADERSIHDFCLVSKVVGRCRSMRWYNTDGSQQLFVYGGCDGNSNNYLTKECLKK 60
 DB 19 ADERSIHDFCLVSKVVGRCRSMRWYNTDGSQQLFVYGGCDGNSNNYLTKECLKK 78
 QY 61 CATVTENATGDLATSRNAADSSVPSAPRRQDSHSDMFNVEYCTANAVTGPCRASFP 120
 DB 79 CATVTENATGDLATSRNAADSSVPSAPRRQDSHSDMFNVEYCTANAVTGPCRASFP 138
 QY 121 RWYFDVERNSCNNFIYGGCRGNKNSYRSEACMLRCFRQENPPLPLGSK 170
 DB 139 RWYFDVERNSCNNFIYGGCRGNKNSYRSEACMLRCFRQENPPLPLGSK 188
 RESULT 7
 AAB14160
 ID AAB14160 standard; protein; 197 AA.
 XX AC AAB14160;
 XX 02-FEB-2001 (first entry)
 XX DE Human placental bikunin mature protein and signal peptide.
 XX Human; mucociliary dysfunction; mucus; sputum;
 KW chronic obstructive lung disease; chronic bronchitis; CB; Bronchiectasis;

KW BE; asthma; cystic fibrosis; CF; bacterial infection; placental bikunin;
 KW Kunitz-type serine protease inhibitor; chronic sinusitis; glue ear.
 XX
 OS Homo sapiens.
 FH Key Location/Qualifiers
 FT Peptide 1..18
 FT Protein /label= Signal_peptide
 FT 19..197
 FT /label= Mature_protein
 XX
 PN WO200037099-A2.
 XX
 PD 29-JUN-2000.
 XX
 PF 22-DEC-1999; 99WO-GB04381.
 XX
 PR 22-DEC-1998; 98US-0218913.
 PR 17-NOV-1999; 99US-0441966.
 XX
 PA (FARB) BAYER AG.
 XX
 PI Hall R, Poll CT, Newton BB, Taylor WJA;
 XX
 DR WPI; 2000-452127/39.
 XX
 PT Stimulating mucociliary clearance rate of mucus and sputum in lung
 PT ways for treating lung diseases such as cystic fibrosis and
 PT bronchitis involves administering a Kunitz-type serine protease
 PT inhibitor -
 XX
 PS Claim 13; Page 88; 173pp; English.
 XX
 CC Mucociliary dysfunction is the inability of ciliated epithelium to clear
 CC mucus and sputum in lung airways. Mucociliary dysfunction is a serious
 CC complication of chronic obstructive lung diseases such as Chronic
 CC Bronchitis (CB), Bronchiectasis (BE), asthma and Cystic Fibrosis (CF).
 CC In addition, patients suffering from mucociliary dysfunction are
 CC susceptible to secondary bacterial infections. The present sequence is
 CC human placental bikunin. This protein is a Kunitz-type serine protease
 CC inhibitor protein, which can stimulate the rate of mucociliary clearance
 CC of mucus and sputum in lung airways. Therefore, the present protein may
 CC be used for treating lung diseases such as CF, CB, BE, and chronic
 CC sinusitis and glue ear which are caused by retention and accumulation of
 CC mucus. The present sequence is the full-length human placental bikunin
 CC protein sequence.
 XX
 SQ Sequence 197 AA;
 Query Match 100.0%; Score 948; DB 21; Length 197;
 Best Local Similarity 100.0%; Pred. No. 4.8e-89;
 Matches 170; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ADERSIHDFCLVSKVVGRCRSMRPWWNVTDGSCQLFVYGGCDGNSNNYLTKECLKK 60
 DB 19 ADERSIHDFCLVSKVVGRCRSMRPWWNVTDGSCQLFVYGGCDGNSNNYLTKECLKK 78
 QY 61 CATVTENATGDLATSRNAADSSVPSAPRRQDSHSDMFNVEEYCTANAVTGPCRASFP 120
 DB 79 CATVTENATGDLATSRNAADSSVPSAPRRQDSHSDMFNVEEYCTANAVTGPCRASFP 138
 QY 121 RWFYDVERNSCNFIYGGCRGNKNSYRSEACMLRCFRQENPPLPLGSK 170
 DB 139 RWFYDVERNSCNFIYGGCRGNKNSYRSEACMLRCFRQENPPLPLGSK 188
 RESULT 8
 ID AAW30042
 XX AAW30042 standard; Protein; 213 AA.
 AC AAW30042;
 XX
 DT 20-APR-1998 (first entry)

XX DE Human placental bikunin.
 XX
 KW Human; placental bikunin; inhibition; trypsin; kallikrein;
 KW plasmin; factor XIIa; treatment; prevention; oedema;
 KW inflammation; infection; granulomatosis; multiple sclerosis;
 KW ischaemia; perioperative blood loss; sepsis; shock; fibrosis;
 KW blood coagulation disease; polytrauma; stroke; haemorrhage;
 KW gastric cancer; cervical cancer; metastasis; blood loss.
 XX
 OS Homo sapiens.
 XX
 PN WO9733996-A2.
 XX
 PD 18-SEP-1997.
 XX
 PF 10-MAR-1997; 97WO-US03894.
 XX
 PR 04-OCT-1996; 96US-0725251.
 PR 11-MAR-1996; 96US-0013106.
 PR 14-JUN-1996; 96US-0019793.
 XX
 PA (FARB) BAYER CORP.
 XX
 PI Davis G, Delaria KA, Marlor CW, Muller DK, Tamburini PP;
 XX
 DR WPI; 1997-470876/43.
 XX
 PT New human placental bikunin - used to inhibit kallikrein, trypsin
 PT etc. in treatment of oedema, multiple sclerosis, fibrosis, or
 PT perioperative blood loss
 XX
 PS Claim 1; Page 65; 110pp; English.
 XX
 CC The present sequence is a human placental bikunin, which
 CC inhibits, e.g. trypsin, kallikrein, plasmin and factor XIIa.
 CC Bikunin can be used to treat or prevent brain and spinal cord
 CC oedema, inflammation, infection or granulomatosis, multiple
 CC sclerosis, ischaemia, perioperative blood loss, sepsis, shock,
 CC fibrosis, blood coagulation diseases, polytrauma, stroke,
 CC cerebral or subarachnoid haemorrhage and gastric or cervical
 CC cancer and prevent metastasis. It is particularly useful for
 CC reducing blood loss during surgery, and can also be used to treat
 CC other cancer, arthritis, anaemia, non-insulin dependent diabetes,
 CC influenza and similar viral infections, acute pancreatitis and
 CC gout, and prevent pre-term labour. It has similar properties to
 CC aprotinin, but is less highly charged so should be less
 CC immunogenic and less likely to damage the kidneys. Manipulation
 CC of the bikunin sequence may allow the inhibitory profile to be
 CC altered. It also reduces or eliminates the need for whole donor
 CC blood or blood products during surgery, thereby reducing the risk
 CC of infection and other adverse side effects, as well as reducing
 CC the cost of surgery.
 XX
 SQ Sequence 213 AA;
 Query Match 100.0%; Score 948; DB 18; Length 213;
 Best Local Similarity 100.0%; Pred. No. 5.3e-89;
 Matches 170; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ADERSIHDFCLVSKVVGRCRSMRPWWNVTDGSCQLFVYGGCDGNSNNYLTKECLKK 60
 DB 1 ADERSIHDFCLVSKVVGRCRSMRPWWNVTDGSCQLFVYGGCDGNSNNYLTKECLKK 60
 QY 61 CATVTENATGDLATSRNAADSSVPSAPRRQDSHSDMFNVEEYCTANAVTGPCRASFP 120
 DB 61 CATVTENATGDLATSRNAADSSVPSAPRRQDSHSDMFNVEEYCTANAVTGPCRASFP 120
 QY 121 RWFYDVERNSCNFIYGGCRGNKNSYRSEACMLRCFRQENPPLPLGSK 170
 DB 121 RWFYDVERNSCNFIYGGCRGNKNSYRSEACMLRCFRQENPPLPLGSK 170

RESULT 9
AAB14184
ID AAB14184 standard; protein; 213 AA.
AC AAB14184;
XX
DT 02-FEB-2001 (first entry)
XX
DE Human placental bikunin protein # 2.
XX
DE Human; mucociliary dysfunction; mucus; sputum;
KW chronic obstructive lung disease; chronic bronchitis; CB; Bronchiectasis;
KW BE; asthma; cystic fibrosis; CF; bacterial infection; placental bikunin;
KW Kunitz-type serine protease inhibitor; chronic sinusitis; glue ear.
XX
OS Homo sapiens.
XX
PN WO200037099-A2.
XX
PD 29-JUN-2000.
XX
PD 22-DEC-1999; 99WO-GB04381.
XX
PF 22-DEC-1998; 98US-0218913.
PR 17-NOV-1999; 99US-0441966.
XX
PA (FARB) BAYER AG.
XX
PI Hall R, Poll CT, Newton BB, Taylor WJA;
XX
DR WPI; 2000-452127/39.
XX
PT Stimulating mucociliary clearance rate of mucus and sputum in lung
PT airways for treating lung diseases such as cystic fibrosis and
PT bronchitis involves administering a Kunitz-type serine protease
PT inhibitor
XX
PS Disclosure; Page 162; 173pp; English.
XX
CC Mucociliary dysfunction is the inability of ciliated epithelium to clear
CC mucus and sputum in lung airways. Mucociliary dysfunction is a serious
CC complication of chronic obstructive lung diseases such as Chronic
CC Bronchitis (CB), Bronchiectasis (BE), asthma and Cystic Fibrosis (CF).
CC In addition, patients suffering from mucociliary dysfunction are
CC susceptible to secondary bacterial infections. The present sequence is a
CC fragment of human placental bikunin. Human placental bikunin is a
CC Kunitz-type serine protease inhibitor protein, which can stimulate the
CC rate of mucociliary clearance of mucus and sputum in lung airways.
CC Therefore, the present protein fragment may be used for treating lung
CC diseases such as CF, CB, BE, and chronic sinusitis and glue ear which
CC are caused by retention and accumulation of mucus.
CC Note: the present sequence is defined as SEQ ID 46 in the sequence
CC listing. However, in figure 4E of the specification, SEQ ID 46 is
CC clearly shown as a nucleotide sequence. Therefore, the nucleotide
CC sequence has been described in AAA70393.
XX
SQ Sequence 213 AA;
Query Match 100.0%; Score 948; DB 21; Length 213;
Best Local Similarity 100.0%; Pred. No. 5.3e-89;
Matches 170; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ADERSIHDFCLVSKVVGRCRAMPWWYNVTDGSCQLFVYGGCDGNSNNYLTKECLKK 60
Db 1 ADERSIHDFCLVSKVVGRCRAMPWWYNVTDGSCQLFVYGGCDGNSNNYLTKECLKK 60
QY 61 CATVTENATGDLATSRNAADSSVPSAPRRQDSEDHSSDMFNFEYCTANAVTGPCRASFP 120
Db 61 CATVTENATGDLATSRNAADSSVPSAPRRQDSEDHSSDMFNFEYCTANAVTGPCRASFP 120
QY 121 RWFYDVERNSCNFNFIYGGCRGNKNSYRSEACMLRCFROQENPPLPLGSK 170
Db 121 RWFYDVERNSCNFNFIYGGCRGNKNSYRSEACMLRCFROQENPPLPLGSK 170

RESULT 10
AAB14200
ID AAB14200 standard; protein; 213 AA.
XX
AC AAB14200;
XX
DT 02-FEB-2001 (first entry)
XX
DE Human placental bikunin protein fragment # 15.
XX
DE Human; mucociliary dysfunction; mucus; sputum;
KW chronic obstructive lung disease; chronic bronchitis; CB; Bronchiectasis;
KW BE; asthma; cystic fibrosis; CF; bacterial infection; placental bikunin;
KW Kunitz-type serine protease inhibitor; chronic sinusitis; glue ear.
XX
OS Homo sapiens.
XX
PN WO200037099-A2.
XX
PD 29-JUN-2000.
XX
PF 22-DEC-1999; 99WO-GB04381.
PR 22-DEC-1998; 98US-0218913.
PR 17-NOV-1999; 99US-0441966.
XX
PA (FARB) BAYER AG.
XX
PI Hall R, Poll CT, Newton BB, Taylor WJA;
XX
DR WPI; 2000-452127/39.
XX
PT Stimulating mucociliary clearance rate of mucus and sputum in lung
PT airways for treating lung diseases such as cystic fibrosis and
PT bronchitis involves administering a Kunitz-type serine protease
PT inhibitor
XX
PS Claim 13; Page 88; 173pp; English.
XX
CC Mucociliary dysfunction is the inability of ciliated epithelium to clear
CC mucus and sputum in lung airways. Mucociliary dysfunction is a serious
CC complication of chronic obstructive lung diseases such as Chronic
CC Bronchitis (CB), Bronchiectasis (BE), asthma and Cystic Fibrosis (CF).
CC In addition, patients suffering from mucociliary dysfunction are
CC susceptible to secondary bacterial infections. The present sequence is a
CC fragment of human placental bikunin. Human placental bikunin is a
CC Kunitz-type serine protease inhibitor protein, which can stimulate the
CC rate of mucociliary clearance of mucus and sputum in lung airways.
CC Therefore, the present protein fragment may be used for treating lung
CC diseases such as CF, CB, BE, and chronic sinusitis and glue ear which are
CC caused by retention and accumulation of mucus.
XX
SQ Sequence 213 AA;
Query Match 100.0%; Score 948; DB 21; Length 213;
Best Local Similarity 100.0%; Pred. No. 5.3e-89;
Matches 170; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ADERSIHDFCLVSKVVGRCRAMPWWYNVTDGSCQLFVYGGCDGNSNNYLTKECLKK 60
Db 1 ADERSIHDFCLVSKVVGRCRAMPWWYNVTDGSCQLFVYGGCDGNSNNYLTKECLKK 60
QY 61 CATVTENATGDLATSRNAADSSVPSAPRRQDSEDHSSDMFNFEYCTANAVTGPCRASFP 120
Db 61 CATVTENATGDLATSRNAADSSVPSAPRRQDSEDHSSDMFNFEYCTANAVTGPCRASFP 120
QY 121 RWFYDVERNSCNFNFIYGGCRGNKNSYRSEACMLRCFROQENPPLPLGSK 170
Db 121 RWFYDVERNSCNFNFIYGGCRGNKNSYRSEACMLRCFROQENPPLPLGSK 170

RESULT 11	DB	61	CATVTENATGDLATSRNAADSSVPSAPRRQDSHSDMFNEEYCTANAVTGPCRASFP	120
AAW30046	QY	121	RWYFVERNSCNFIYGGCGNKNYSRSEACMLRCFRQOENPPLGSK	170
ID AAW30046 standard; Protein; 225 AA.	DB	121	RWYFVERNSCNFIYGGCGNKNYSRSEACMLRCFRQOENPPLGSK	170
AC AAW30046;				
XX				
DT 20-APR-1998 (first entry)				
XX				
DE Human placental bikunin.				
XX				
XX Human; placental bikunin; inhibition; trypsin; kallikrein;				
KW plasmin; factor XIIa; treatment; prevention; oedema;				
KW inflammation; infection; granulomatosis; multiple sclerosis;				
KW ischaemia; perioperative blood loss; sepsis; shock; fibrosis;				
KW blood coagulation disease; polytrauma; stroke; haemorrhage;				
KW gastric cancer; cervical cancer; metastasis; blood loss.				
XX				
OS Homo sapiens.				
XX				
PN WO9733996-A2.				
XX				
PD 18-SEP-1997.				
XX				
PF 10-MAR-1997; 97WO-US03894.				
XX				
PR 04-OCT-1996; 96US-0725251.				
PR 11-MAR-1996; 96US-0013106.				
PR 14-JUN-1996; 96US-0019793.				
XX				
PA (FARB) BAYER CORP.				
XX				
PI Davis G, Delaria KA, Marlor CW, Muller DK, Tamburini PP;				
XX				
DR WPI; 1997-470876/43.				
XX				
PT New human placental bikunin - used to inhibit kallikrein, trypsin				
PT etc. in treatment of oedema, multiple sclerosis, fibrosis, or				
PT perioperative blood loss				
XX				
PS Claim 1; Page 66; 110pp; English.				
XX				
CC The present sequence is a human placental bikunin, which				
CC inhibits, e.g. trypsin, kallikrein, plasmin and factor XIIa.				
CC Bikunin can be used to treat or prevent brain and spinal cord				
CC oedema, inflammation, infection or granulomatosis, multiple				
CC sclerosis, ischaemia, perioperative blood loss, sepsis, shock,				
CC fibrosis, blood coagulation diseases, polytrauma, stroke,				
CC cerebral or subarachnoid haemorrhage and gastric or cervical				
CC cancer and prevent metastasis. It is particularly useful for				
CC reducing blood loss during surgery, and can also be used to treat				
CC other cancer, arthritis, anaemia, non-insulin dependent diabetes,				
CC influenza and similar viral infections, acute pancreatitis and				
CC gout, and prevent pre-term labour. It has similar properties to				
CC aprotinin, but is less highly charged so should be less				
CC immunogenic and less likely to damage the kidneys. Manipulation				
CC of the bikunin sequence may allow the inhibitory profile to be				
CC altered. It also reduces or eliminates the need for whole donor				
CC blood or blood products during surgery, thereby reducing the risk				
CC of infection and other adverse side effects, as well as reducing				
CC the cost of surgery.				
XX				
SQ Sequence 225 AA;				
Query Match		100.0%;	Score 948;	DB 18; Length 225;
Best Local Similarity		100.0%;	Pred. No. 5.7e-89;	
Matches	170;	Conservative	0;	Mismatches 0; Indels 0; Gaps 0;
QY	1	ADRSRSHDFCLVSKVVGRCRSMRPWWNVTDGSCQLFVYGGCDGNSNNYLTKECLKK	60	
DB	1	ADRSRSHDFCLVSKVVGRCRSMRPWWNVTDGSCQLFVYGGCDGNSNNYLTKECLKK	60	
QY	61	CATVTENATGDLATSRNAADSSVPSAPRRQDSHSDMFNEEYCTANAVTGPCRASFP	120	

QY 61 CATVTENATGDLATSRNAADSSVPSAPRRQDSHSDMFNEEYCTANAVTGPCRASEP 120
|||||
Db 61 CATVTENATGDLATSRNAADSSVPSAPRRQDSHSDMFNEEYCTANAVTGPCRASEP 120
|||||
QY 121 RWYFDVERNSCNFFIYGGCRGNKNSYRSEACMLRCFROQENPPLPLGSK 170
|||||
Db 121 RWYFDVERNSCNFFIYGGCRGNKNSYRSEACMLRCFROQENPPLPLGSK 170
|||||
RESULT 13
AAB14201
ID AAB14201 standard; protein; 225 AA.
XX
AC AAB14201;
XX
DT 02-FEB-2001 (first entry)
XX
DE Human placental bikunin protein fragment # 16.
XX
KW Human; mucociliary dysfunction; mucus; sputum;
KW chronic obstructive lung disease; chronic bronchitis; CB; Bronchiectasis;
KW BE; asthma; cystic fibrosis; CF; bacterial infection; placental bikunin;
KW Kunitz-type serine protease inhibitor; chronic sinusitis; glue ear.
XX
OS Homo sapiens.
XX
PN W0200037099-A2.
XX
PD 29-JUN-2000.
XX
PF 22-DEC-1999; 99WO-G804381.
XX
PR 22-DEC-1998; 98US-0218913.
PR 17-NOV-1999; 99US-0441966.
XX
PA (FARB) BAYER AG.
XX
PI Hall R, Poll CT, Newton BB, Taylor WJA;
XX
PD WPI; 2000-452127/39.
XX
PF Stimulating mucociliary clearance rate of mucus and sputum in lung
PT airways for treating lung diseases such as cystic fibrosis and
PT bronchitis involves administering a Kunitz-type serine protease
PT inhibitor
XX
PS Claim 13; Pages 88-89; 173pp; English.
XX
CC Mucociliary dysfunction is the inability of ciliated epithelium to clear
CC mucus and sputum in lung airways. Mucociliary dysfunction is a serious
CC complication of chronic obstructive lung diseases such as Chronic
CC Bronchitis (CB), Bronchiectasis (BE), asthma and Cystic Fibrosis (CF).
CC In addition, patients suffering from mucociliary dysfunction are
CC susceptible to secondary bacterial infections. The present sequence is a
CC fragment of human placental bikunin. Human placental bikunin is a
CC Kunitz-type serine protease inhibitor protein, which can stimulate the
CC rate of mucociliary clearance of mucus and sputum in lung airways.
CC Therefore, the present protein fragment may be used for treating lung
CC diseases such as CF, CB, BE, and chronic sinusitis and glue ear which are
CC caused by retention and accumulation of mucus.
XX
SQ Sequence 225 AA;
Query Match 100.0%; Score 948; DB 21; Length 225;
Best Local Similarity 100.0%; Pred. No. 5.7e-89;
Matches 170; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ADERSIHDFCLVSKVVGRCRAMPWWYNVTGDSQQLFVYGGCDGNSNNYLTKECLKK 60
|||||
Db 1 ADERSIHDFCLVSKVVGRCRAMPWWYNVTGDSQQLFVYGGCDGNSNNYLTKECLKK 60
|||||
QY 61 CATVTENATGDLATSRNAADSSVPSAPRRQDSHSDMFNEEYCTANAVTGPCRASEP 120
|||||

Db 61 CATVTENATGDLATSRNAADSSVPSAPRRQDSHSDMFNEEYCTANAVTGPCRASEP 120
QY 121 RWYFDVERNSCNFFIYGGCRGNKNSYRSEACMLRCFROQENPPLPLGSK 170
|||||
Db 121 RWYFDVERNSCNFFIYGGCRGNKNSYRSEACMLRCFROQENPPLPLGSK 170
|||||
RESULT 14
AAW30060
ID AAW30060 standard; Protein; 235 AA.
XX
AC AAW30060;
XX
DT 20-APR-1998 (first entry)
XX
DE Human consensus bikunin.
XX
KW Human; consensus bikunin; inhibition; trypsin; kallikrein;
KW plasmin; factor XIIa; treatment; prevention; oedema;
KW inflammation; infection; granulomatosis; multiple sclerosis;
KW ischaemia; perioperative blood loss; sepsis; shock; fibrosis;
KW blood coagulation disease; polytrauma; stroke; haemorrhage;
KW gastric cancer; cervical cancer; metastasis; blood loss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Misc-difference 198 /note= "encoded by TGA"
FT Misc-difference 201 /note= "encoded by TGA"
FT Misc-difference 226 /note= "encoded by GAN"
FT Misc-difference 233 /note= "encoded by TGA"
XX
PN W09733996-A2.
XX
PD 18-SEP-1997.
XX
PF 10-MAR-1997; 97WO-US03894.
XX
PR 04-OCT-1996; 96US-0725251.
PR 11-MAR-1996; 96US-0013106.
PR 14-JUN-1996; 96US-0019793.
XX
PA (FARB) BAYER CORP.
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PI Davis G, Delaria KA, Marlor CW, Muller DK, Tamburini PP;
XX
PD WPI: 1997-470876/43.
DR N-PSDB; AAT90732.
XX
PT New human placental bikunin - used to inhibit kallikrein, trypsin
PT etc. in treatment of oedema, multiple sclerosis, fibrosis, or
PT perioperative blood loss
XX
PS Disclosure; Fig 3; 110pp; English.
XX
CC The present sequence is a consensus human bikunin, which
CC inhibits, e.g. trypsin, kallikrein, plasmin and factor XIIa.
CC Bikunin can be used to treat or prevent brain and spinal cord
CC oedema, inflammation, infection or granulomatosis, multiple
CC sclerosis, ischaemia, perioperative blood loss, sepsis, shock,
CC fibrosis, blood coagulation diseases, polytrauma, stroke,
CC cerebral or subarachnoid haemorrhage and gastric or cervical
CC cancer and prevent metastasis. It is particularly useful for
CC reducing blood loss during surgery, and can also be used to treat
CC other cancer, arthritis, anaemia, non-insulin dependent diabetes,
CC influenza and similar viral infections, acute pancreatitis and
CC gout, and prevent pre-term labour. It has similar properties to
CC aprotinin, but is less highly charged so should be less
CC immunogenic and less likely to damage the kidneys. Manipulation

